

GenCore version 5.1.6  
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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: January 5, 2006, 16:07:38 ; Search time 4844 Seconds

(without alignments)  
2522.986 Million cell updates/sec

Title: US-09-977-579A-2

Perfect score: 1124

Sequence: 1 MPANRRLPLASLVIYWS.....SDYLAIPSENKENSAPVPEE 215

Scoring table:

BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 5883141 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

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-O=/cgn2\_1/USPTO\_spool/US09977579/runat\_05012006\_160652\_29018/app\_query.fasta\_1.391  
-DB=GenEmbl -QMT=fastcap -SUFFIX=rge -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0  
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45  
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-NO\_MMAP -LARGEQUERY -NEG\_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG  
-DEV\_TIMEOUT=120 -WARN\_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

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1: gb.ba.\*  
2: gb.in.\*  
3: gb.env.\*  
4: gb.om.\*  
5: gb.ov.\*  
6: gb.pat.\*  
7: gb.ph.\*  
8: gb.pr.\*  
9: gb.ro.\*  
10: gb.sts.\*  
11: gb.sy.\*  
12: gb.un.\*  
13: gb.vi.\*  
14: gb.htg.\*  
15: gb.pl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1124	100.0	1261	6	AR359850 Sequence
2	1124	100.0	1261	6	AX039100 Sequence
3	1124	100.0	1261	8	AJ243396 Homo sapi

4	1124	100.0	5306	8	AB032984	AB032984 Homo sapi
5	1116	99.3	3296	8	AB097521	AB097521 Macaca fa
6	1105	98.3	645	6	AX048004	AX048004 Sequence
7	1105	98.3	2220	6	AR359849	AR359849 Sequence
8	1105	98.3	2220	6	AX039099	AX039099 Sequence
9	1105	98.3	2220	6	RNO243395	AJ243395 Rattus no
10	1105	98.3	2632	6	AX048005	AX048005 Sequence
11	1105	98.3	3107	9	AF378093	AF378093 Rattus no
12	1105	98.3	3108	6	AX047984	AX047984 Sequence
13	1105	98.3	3910	9	BC070899	BC070899 Rattus no
14	1097	97.6	4025	9	AK173115	AK173115 Mus muscu
15	1097	97.6	4169	9	BC053919	BC053919 Mus muscu
16	1097	97.6	4176	9	BC058636	BC058636 Mus muscu
17	1091	97.1	670	9	AY049036	AY049036 Mus muscu
18	1028	91.5	606	6	CQ728741	CQ728741 Sequence
19	857	76.2	922	5	BX935227	BX935227 Gallus ga
20	755	67.2	912	5	BX931708	BX931708 Gallus ga
21	743	66.1	1736	5	BC088017	BC088017 Xenopus t
22	742	66.0	471	6	BD059018	BD059018 Secreted
23	714	63.5	1654	5	BC077295	BC077295 Xenopus l
24	477	42.4	657	4	OCU35382	U35382 Oryctolagus
25	477	42.4	657	6	AX048006	AX048006 Sequence
26	473	42.1	1335	8	HUMVSC1B	L16242 Homo sapien
27	473	42.1	1404	8	HUMSCN1BA	L10338 Human sodiu
28	473	42.1	1525	8	BC067122	BC067122 Homo sapi
29	472	42.0	701	4	DQ061859	DQ061859 Canis fam
30	472	42.0	1490	6	AX01978	AX01978 Sequence
31	472	42.0	1490	9	RATSCH1B	M91808 Rattus norv
32	472	42.0	1527	9	BC094523	BC094523 Rattus no
33	471	41.9	657	8	BT019923	BT019923 Homo sapi
34	471	41.9	657	11	AY888280	AY888280 Synthetic
35	471	41.9	1557	9	BC039140	BC039140 Mus muscu
36	470	41.8	617	6	CQ722293	CQ722293 Sequence
37	468	41.6	1125	9	MMU46681	U46681 Mus musculu
38	468	41.6	1340	9	MMU85786	U85786 Mus musculu
39	468	41.6	1568	9	BC009652	BC009652 Mus muscu
40	423	37.6	1239	8	BC021266	BC021266 Homo sapi
41	400.5	35.6	132290	9	AC135353	AC135353 Mus muscu
42	400.5	35.6	174285	14	AC145484	AC145484 Lemur cat
43	400.5	35.6	238861	14	AC148331	AC148331 Mus muscu
44	400	35.6	214306	14	AC128723	AC128723 Rattus no
45	398.5	35.5	286712	14	AC157079	AC157079 Bos tauru

#### ALIGNMENTS

RESULT 1	AR359850	Sequence 4 from patent US 6593565.	1261 bp.	DNA	linear	PAT 17-AUG-2003
LOCUS	AR359850	Sequence 4 from patent US 6593565.	1261 bp.	DNA	linear	PAT 17-AUG-2003
DEFINITION	AR359850	Sequence 4 from patent US 6593565.	1261 bp.	DNA	linear	PAT 17-AUG-2003
ACCESSION	AR359850	Sequence 4 from patent US 6593565.	1261 bp.	DNA	linear	PAT 17-AUG-2003
VERSION	AR359850.1	GI:33766660				
KEYWORDS	Unknown.					
SOURCE	Unknown.					
ORGANISM	Unclassified.					
REFERENCE	1 (bases 1 to 1261)					
AUTHORS	Heslin,P. and Lynam,N.R.					
TITLE	Vehicle interior rearview mirror assembly including an accessory-containing housing					
JOURNAL	Patent: US 6593565-A 4 15-JUL-2003;					
FEATURES	Donnelly Corporation; Holland, MI					
source	Location/Qualifiers					
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	/mol_type="genomic DNA"					

#### ORIGIN

Alignment Scores:	2.78e-117	Length:	1261
Pred. No.:	1124.00	Matches:	215
Score:	100.00%	Conservative:	0
Percent Similarity:	100.00%	Mismatches:	0
Best Local Similarity:	100.00%		

Query Match: DB:	100.00% 6	Indels: Gaps:	0 0
US-09-977-579A-2 (1-215) x AR359850 (1-1261)			
Qy	1	MetProAlaPheAnArgLeuPheProLeuAlaSerLeuValLeuIleTyrTrpValSer	20
Db	376	ATGCTGCTTCAATAGATTGTTCCCTGCTTCTCTCGTGCTTATCTACTGGGTCAGT	435
Qy	21	ValCysPheProValCysValGluValProSerGluThrGluAlaValGlnGlyAsnPro	40
Db	436	GTCTGCTTCCCTGTGTGGAGTGCCTCGGAGACGGAGCGCTGCAGGCAACCC	495
Qy	41	MetLysLeuArgCysIleSerCysMetLysArgGluValGluAlaThrThrValVal	60
Db	496	ATGAAGCTGGCTGCATCTCTGTCATGAAGAGAGAGAGGTGGAGGCCACACCGTGGTG	555
Qy	61	GluTrpPheTyrArgProGluGlyGlyLysAspPheLeuIleTyrGluTyrArgAsnGly	80
Db	556	GAATGGTTCTACAGCCCGAGCGGTAAAGATTTCCTTATTACGAGTATCGGAATGCG	615
Qy	81	HisGlnGluValGluSerProPheGlnGlyArgLeuGlnTrpAsnGlySerLysAspLeu	100
Db	616	CACCAGGAGGTGGAGAGCCCTTTTCAGGGCGCTGCAGTGAATGGCAGCAAGACCTG	675
Qy	101	GlnAspValSerIleThrValLeuAsnValThrLeuAsnAspSerGlyLeuTyrThrCys	120
Db	676	CAGGACGTGTCCATCACTGTCTCAACGTCACTCTGAACGACTCTCGGCTCTACACCTGC	735
Qy	121	AsnValSerArgGluPheGluPheGluAlaHisArgProPheValLysThrThrArgLeu	140
Db	736	AATGTGTCCTCCGGAGTTTGAGTTTGAGCGCATCGCCCTTTGTGAACACGACCGGCTG	795
Qy	141	IleProLeuArgValThrGluAlaGlyGluAspPheThrSerValSerGluIle	160
Db	796	ATCCCCCTAAGAGTCACCGAGGAGCTGGAGAGACTTCACCTCTGTGTCTCAGAAATC	855
Qy	161	MetMetTyrIleLeuLeuValPheLeuThrLeuTrpLeuLeuIleGluMetIleTyrCys	180
Db	856	ATGATGTACATCTCTGCTTCTCCTCACCTGTGGCTCTCATCGAGATGATATATTGC	915
Qy	201	IleProSerGluAsnLysGluAsnSerAlaValProValGluGlu	215
Db	976	ATCCCATCTGAGAACAGAGAACTCTGCGGTACCACTGGAGGAA	1020
RESULT 2			
AX039100		1261 bp	DNA linear PAT 18-NOV-2000
LOCUS	Sequence 4 from Patent WO0063367.		
DEFINITION	AX039100		
ACCESSION	AX039100.1	GI:11229276	
VERSION			
KEYWORDS			
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;		
	Hominidae; Homo.		
REFERENCE			
AUTHORS	1		
TITLE	Cox, P., Dixon, A., Jackson, A. and Morgan, K.		
	A novel family of beta sub-unit proteins from a voltage-gated sodi		
	um channel, nucleic acids encoding them and therapeutic or		
	diagnostic uses thereof		
JOURNAL	Patent: WO 0063367-A 4 26-OCT-2000;		
	WARNER-LAMBERT COMPANY (US) ; Cambridge University Technical		
	Services Limited (GB)		
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Alignment Scores:			
Pred. No.:	2.78e-117	Length:	1261
Score:	1124.00	Matches:	215
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	6	Gaps:	0
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Qy	21	ValCysPheProValCysValGluValProSerGluThrGluAlaValGlnGlyAsnPro	40
Db	436	GTCTGCTTCCCTGTGTGGAGTGCCTCGGAGACGGAGCGCTGCAGGCAACCC	495
Qy	41	MetLysLeuArgCysIleSerCysMetLysArgGluValGluAlaThrThrValVal	60
Db	496	ATGAAGCTGGCTGCATCTCTGTCATGAAGAGAGAGAGGTGGAGGCCACACCGTGGTG	555
Qy	61	GluTrpPheTyrArgProGluGlyGlyLysAspPheLeuIleTyrGluTyrArgAsnGly	80
Db	556	GAATGGTTCTACAGCCCGAGCGGTAAAGATTTCCTTATTACGAGTATCGGAATGCG	615
Qy	81	HisGlnGluValGluSerProPheGlnGlyArgLeuGlnTrpAsnGlySerLysAspLeu	100
Db	616	CACCAGGAGGTGGAGAGCCCTTTTCAGGGCGCTGCAGTGAATGGCAGCAAGACCTG	675
Qy	101	GlnAspValSerIleThrValLeuAsnValThrLeuAsnAspSerGlyLeuTyrThrCys	120
Db	676	CAGGACGTGTCCATCACTGTCTCAACGTCACTCTGAACGACTCTCGGCTCTACACCTGC	735
Qy	121	AsnValSerArgGluPheGluPheGluAlaHisArgProPheValLysThrThrArgLeu	140
Db	736	AATGTGTCCTCCGGAGTTTGAGTTTGAGCGCATCGCCCTTTGTGAACACGACCGGCTG	795
Qy	141	IleProLeuArgValThrGluAlaGlyGluAspPheThrSerValSerGluIle	160
Db	796	ATCCCCCTAAGAGTCACCGAGGAGCTGGAGAGACTTCACCTCTGTGTCTCAGAAATC	855
Qy	161	MetMetTyrIleLeuLeuValPheLeuThrLeuTrpLeuLeuIleGluMetIleTyrCys	180
Db	856	ATGATGTACATCTCTGCTTCTCCTCACCTGTGGCTCTCATCGAGATGATATATTGC	915
Qy	181	TyrArgLysValSerLysAlaGluAlaGlnGluAsnAlaSerAspTyrLeuAla	200
Db	916	TACAGAAAGGTCTCAAAAGCCGAGAGACGCCCAAGAAACGGCTCTGACTACTCTGCC	975
Qy	201	IleProSerGluAsnLysGluAsnSerAlaValProValGluGlu	215
Db	976	ATCCCATCTGAGAACAGAGAACTCTGCGGTACCACTGGAGGAA	1020
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LOCUS	Sequence 4 from Patent WO0063367.		
DEFINITION	AX039100		
ACCESSION	AX039100.1	GI:7242612	
VERSION			
KEYWORDS			
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;		
	Hominidae; Homo.		
REFERENCE			
AUTHORS	1		
TITLE	Cox, P., Dixon, A., Jackson, A. and Morgan, K.		
	A novel family of beta sub-unit proteins from a voltage-gated sodi		
	um channel, nucleic acids encoding them and therapeutic or		
	diagnostic uses thereof		
JOURNAL	Patent: WO 0063367-A 4 26-OCT-2000;		
	WARNER-LAMBERT COMPANY (US) ; Cambridge University Technical		
	Services Limited (GB)		
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source	1. .1261		
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	/mol_type="unassigned DNA"		

Jackson, A.P.  
beta 3: an additional auxiliary subunit of the voltage-sensitive sodium channel that modulates channel gating with distinct kinetics  
Proc. Natl. Acad. Sci. U.S.A. 97 (5), 2308-2313 (2000)  
10688874

2  
Morgan, K.  
Direct Submission  
Submitted (28-JUN-1999) Morgan K., Biochemistry, University of Cambridge, Tennis Court Road, Cambridge, CB2 1QW, UNITED KINGDOM  
Revised by [4]  
3 (bases 1 to 1261)  
Morgan, K.  
Direct Submission  
Submitted (13-MAR-2000) Morgan K., Biochemistry, University of Cambridge, Tennis Court Road, Cambridge, CB2 1QW, UNITED KINGDOM  
On Mar 14, 2000 this sequence version replaced gi:1160974.  
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Alignment Scores:  
Pred. No.: 2,78e-117 Length: 1261  
Score: 1124.00 Matches: 215  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 8 Gaps: 0

US-09-977-579A-2 (1-215) x HSA243396 (1-1261)

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QY 21 ValCysPheProValCysValGluValProSerGluThrGluAlaValGlnGlyAsnPro 40  
Db 436 GTCTGCTTCCCTGTGTGTGGAAAGTCCCTCGAGACGAGGCGGCTGAGGCGCAACCCC 495

QY 41 MetLysLeuArgCysIleSerCysMetLysArgGluGluValGluAlaThrThrValVal 60  
Db 496 ATGAAGCTGGCTGCATCTCTCGTCATGAAGAGAGAGAGAGAGAGAGAGAGAGAGAG 555

QY 61 GluTrpPheTyrArgProGluGlyGlyLysAspPheLeuIleTyrGluTyrArgAsnGly 80  
Db 556 GAATGGTTCTACAGGCCCGGCGGTAAGATTCTCTATTATTCAGGATATCGGAATGGC 615

QY 81 HisGlnGluValGluSerProPheGlnGlyArgLeuGlnTrpAsnGlySerLysAspLeu 100

Db 616 CACCAGAGGTGGAGAGCCCTTTTCAGGGGGCCCTTCAGTGGGAATGGCAGAGACCTG 675  
QY 101 GluAspValSerIleThrValLeuAsnValThrLeuAsnAspSerGlyLeuTyrThrCys 120  
Db 676 CAGGAGGTGTCATCACTGTGCTCAAGTCACTCTGAACGACTCTGGCTCTACACCTGC 735  
QY 121 AsnValSerArgGluPheGluPheGluAlaHisArgProPheValLysThrArgLeu 140  
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QY 201 IleProSerGluAsnLysGluAsnSerAlaValProValGluGlu 215  
Db 976 ATCCCATCTGAGAACAAAGGAGAACTCTGCGGTACCGAGTGGAGGAA 1020

RESULT 4  
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LOCUS Homo sapiens mRNA for KIAA1158 protein, partial cds.  
DEFINITION  
AB032984  
ACCESSION  
AB032984.1 GI:6330135  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
Homo sapiens (human)  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominidae; Homo.  
1 (sites)  
Hirosewa, M., Nagase, T., Ishikawa, K., Kikuno, R., Nomura, N. and  
Ohara, O.  
Characterization of cDNA clones selected by the GeneMark analysis  
from size-fractionated cDNA libraries from human brain  
DNA Res. 6 (5), 329-336 (1999)  
1057461  
2 (bases 1 to 5306)  
Ohara, O., Nagase, T. and Kikuno, R.  
Direct Submission  
Submitted (04-OCT-1999) Osamu Ohara, Kazusa DNA Research Institute,  
Laboratory of DNA Technology, 1532-3 Yana, Kisarazu, Chiba  
292-0812, Japan (E-mail:cdnaifoo@kazusa.or.jp,  
URL: http://www.kazusa.or.jp/huge/, Tel: +81-438-52-3913,  
Fax: +81-438-52-3914)  
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ORIGIN		Alignment Scores:		1.59e-116		Length: 5306	
Pred. No.:		Score:		1124.00		Matches: 215	
Percent Similarity:		100.00%		Conservative: 0			
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Query Match:		100.00%		Indels: 0			
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US-09-977-579A-2 (1-215) x AB032984 (1-5306)							
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Qy	21	ValCysPheProValCysValGluValProSerGluThrGluAlaValGlnGlyAsnPro	40				
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Db	228	GAATGGTTCTACAGGCCGAGGGCGGTAAAGATTTCCTATTACGAGTATCGAATGGC	287				
Qy	81	HisGlnGluValGluSerProPheGlnGlyArgLeuGlnTrpAsnGlySerLysAspLeu	100				
Db	288	CACCAGGAGGTGGAGAGCCCTTTTCAGGGCGCTGCGAGTGAATGGCAGGACCTG	347				
Qy	101	GlnAspValSerIleThrValLeuAsnValThrLeuAsnAspSerGlyLeuTyrThrCys	120				
Db	348	CAGGACGTGTCCATCATCTGTGCTCAACGTCACTCTGAACGACTCTGGCCTCTACAC	407				
Qy	121	AsnValSerArgGluPheGluPheGluAlaHisArgProPheValLysThrThrArgLeu	140				
Db	408	AATGTGTCCGGAGATTGAGTTTGAGCGCATCGGCCCTTTGTGAACAGCAGCGGCTG	467				
Qy	141	IleProLeuArgValThrGluGluAlaGlyGluAspPheThrSerValValSerGluIle	160				
Db	468	ATCCCCCTAAGAGTCACCGAGGAGGCTGGAGAGACTTCACCTCTGTGGTCTCAGAAATC	527				
Qy	161	MetMetTyrIleLeuLeuValPheLeuThrLeuTrpLeuLeuIleGluMetIleTyrCys	180				
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Qy	181	TyrArgLysValSerLysAlaGluGluAlaGlnGluAsnAlaSerAspTyrLeuAla	200				
Db	588	TACAGAAAGGTCTCAAAGCCGAAGAGGACCCCAAGAAACGGCTCTGACTACTTGGC	647				
Qy	201	IleProSerGluAsnLysGluAsnSerAlaValProValGluGlu	215				
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AB097521  
LOCUS  
DEFINITION  
Macaca fascicularis brain cDNA clone:QmoA-13657, similar to human voltage-gated sodium channel beta-3 subunit (SCN3B), mRNA, NM\_018400.  
AB097521  
ACCESSION  
VERSION  
AB097521.1 GI:26449236  
KEYWORDS  
oligo capping; fis (full insert sequence).  
SOURCE  
Macaca fascicularis (crab-eating macaque)  
ORGANISM  
Macaca fascicularis  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Cercopithecoidea; Cercopithecinae; Macaca.  
1  
Ooada,N., Hida,M., Kusuda,J., Tanuma,R., Iseki,K., Hirata,M., Suto,Y., Hirai,M., Terao,K., Suzuki,Y., Sugano,S. and Hashimoto,K. Assignment of 118 novel cDNAs of cynomolgus monkey brain to human chromosomes  
Gene 275 (1), 31-37 (2001)  
11574149  
2 (bases 1 to 3296)  
Hashimoto,K., Ooada,N., Hida,M., Kusuda,J. and Sugano,S. Direct Submission  
Submitted (05-DEC-2002) Katsuyuki Hashimoto, National Institute of Infectious Diseases, Division of Genetic Resources; 23-1, Toyama 1-chome, Shinjuku-ku, Tokyo, 162-8640, Japan  
(E-mail:khashi@nih.go.jp, URL:http://www.nih.go.jp/yoken/genebank/, Tel:81-3-5285-1111(ex.2120), Fax:81-3-5285-1181)  
Lab host: TOP10  
Vector: pME18S-FL3 (Acc.No. AB009864)  
R. Site: DraIII (CACGTGTG)  
R. Site: DraIII (CACGATGG)  
Description: 1st strand cDNA was primed with an oligo(dT) primer using specific 5' and 3' primers and amplified by PCR. The PCR product was digested with SfiI and size selection was performed to exclude fragments <1.5kb. The SfiI-digested PCR product was cloned into distinct draIII sites of pME18S-FL3. XhoI sites just outside the draIII sites can be used to isolate the cDNA insert. Libraries were constructed by oligo-capping method. Custom primers used for sequencing (5' end primer [CTTCTGCTCTAAAGCTGCG]; 3' end primer [CGACCTGCAGCTCGAGCACA]).  
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Alignment Scores:  
Pred. No.: 7,18e-116 Length: 3296  
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Percent Similarity: 99.07% Conservative: 0  
Best Local Similarity: 99.07% Mismatches: 2  
Query Match: 99.29% Indels: 0  
DB: 8 Gaps: 0  
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Qy 21 ValCysPheProValCysValGluValProSerGluThrGluAlaValGlnGlyAsnPro 40  
Db 66 GTCTGCTTCCCGTGTGTGTAAGATGCCCTCGAGACGGAGGTGTGCGAGGCAACCCC 125  
Qy 41 MetLysLeuArgCysIleSerCysMetLysArgGluGluValGluAlaThrThrValVal 60

Db	126	ATGAAGCTGCCTGCATCTCTGATGAGAGAGAGAGGTTGGAGCCACACCGTGGTG	185
Qy	61	GluTrpPheTyrArgProGluGlyGlyLysAspPheLeuIleTyrGluTyrArgAsnGly	80
Db	186	GAATGGTTCTACAGGCCCGAGGGCGGTAAGATTCTTATCTACGAGTATCGGAATGGC	245
Qy	81	HisGlnGluValGluSerProPheGlnGlyArgLeuGlnTrpAsnGlySerLysAspLeu	100
Db	246	CACCAGGAGGTAGAGAGCCCTTTTCAGGGGCGCTGCAGTGGAAATGGACGACCTG	305
Qy	101	GlnAspValSerIleThrValLeuAsnValThrLeuAsnAspSerGlyLysTyrThrCys	120
Db	306	CAGACGTGTCCTCACTGCTCACTCACTCACTCACTCACTCACTCACTCACTCACTG	365
Qy	121	AsnValSerArgGluPheGluAlaHisArgProPheValLysThrArgLeu	140
Db	366	AATGTGTCCTGGAGTTTGGAGCGCATCGGCCCTTTGTGAAGACGACGCGGCTG	425
Qy	141	IleProLeuArgValThrGluAlaGlyGluAspPheThrSerValValSerGluIle	160
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Qy	161	MetMetTyrIleLeuLeuValPheLeuThrLeuTyrLeuLeuIleGluMetIleTyrCys	180
Db	486	ATGATGTACATCTCTCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT	545
Qy	181	TyrArgLysValSerLysAlaGluAlaGlnGluAsnAlaSerAspTyrLeuAla	200
Db	546	TACAGAAAGGTCTCAAAAGCCGAGAGGCGCCCAAGAAACCGCTCTGACTACCTGCC	605
Qy	201	IleProSerGluAsnLysGluAsnSerAlaValProValGluGlu	215
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LOCUS	Sequence 21 from Patent WO0069912.		
DEFINITION	Sequence 21 from Patent WO0069912.		
ACCESSION	AX048004		
VERSION	AX048004.1	GI:11876882	
KEYWORDS	Lepus sp.		
SOURCE	Lepus sp.		
ORGANISM	Lepus sp.		
REFERENCE	1	Curtis, R.A.	
AUTHORS	Gene encoding a sodium channel beta-3 subunit protein		
TITLE	Patent: WO 0069912-A 21 23-NOV-2000;		
JOURNAL	Millennium Pharmaceuticals, Inc. (US)		
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Query Match:	6	Gaps: 0	
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Db      423  GTCTGCTTCCCTGTGTGTGTAAGTGCCTTCGAGACAGAAAGCGGTGCGGGCAATCCC 482
Qy      41   MetLysLeuArgCysIleSerCysMetLysArgGluGluValGluAlaThrThrValVal 60
Db      483  ATGAAGCTGAGTGCAATCTCTCGCATGAAGAGGAGGAGGTGGAGGCCACCACTGTGGTG 542
Qy      61   GluTrpPheTyrArgProGluGlyGlyLysAspPheLeuIleTyrGluTyrArgAsnGly 80
Db      543  GAGTGGTTCACAGCCCTGAGGCGGTAAAGATTCCTTATATAGTAGTATCGGAATGCG 602
Qy      81   HisGlnGluValGluSerProPheGlnGlyArgGluGluTrpAsnGlySerLysAspLeu 100
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Qy      101  GlnAspValSerIleThrValLeuAsnValThrLeuAsnAspSerGlyLeuTyrThrCys 120
Db      663  CAGACGCTATCCATCTACTGACTCAATGTCACTTTGAATGACTCTGGCCTCTACACATGC 722
Qy      121  AsnValSerArgGluPheGluAlaHisArgProPheValLysThrThrArgLeu 140
Db      723  AATGTGTCAGGAGTTCGAATTCGAGGCACACAGGCTTTTGTGAAGACCACGAGACTG 782
Qy      141  IleProLeuArgValThrGluGluAlaGlyGluAspPheThrSerValSerGluIle 160
Db      783  ATACCTTTGGAGTCACTCAAGAGCGGAGAGACTTCACCTCCGTGGTCTCGGAATC 842
Qy      161  MetMetTyrIleLeuLeuValPheLeuThrLeuTrpLeuIleGluMetIleTyrCys 180
Db      843  ATGATGTACATCCCTCCCTGGTCTCCTCACCTTGCTGCTGTTATTTGAGATGATCTATTGC 902
Qy      181  TyrArgLysValSerLysAlaGluGluAlaGlnGluAsnAlaSerAspTyrLeuAla 200
Db      903  TACAGAAAGTCTCTAAGCCGAGAGGCACAGAGAAATGCGTCTGACTACCTTGCT 962

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DEFINITION Sequence 3 from Patent WO0063367.
ACCESSION AX039099
VERSION AX039099.1 GI:11229275
KEYWORDS
SOURCE Rattus sp.
ORGANISM Rattus sp.
REFERENCE
AUTHORS Cox,P., Dixon,A., Jackson,A. and Morgan,K.
TITLE A novel family of beta sub-unit proteins from a voltage-gated sodi
um channel, nucleic acids encoding them and therapeutic or
diagnostic uses there of
JOURNAL Patent: WO 0063367-A 3 26-OCT-2000;
WARNER-LAMBERT COMPANY (US) ; Cambridge University Technical
Services Limited (GB)
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Alignment Scores: 7.85e-115 Length: 2220
Pred. No.: 1105.00 Matches: 211
Score:

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Percent Similarity: 98.14% Conservative: 0
Best Local Similarity: 98.14% Mismatches: 4
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DB: 6 Gaps: 0
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Db      423  GTCTGCTTCCCTGTGTGTGTAAGTGCCTTCGAGACAGAAAGCGGTGCGGGCAATCCC 482
Qy      41   MetLysLeuArgCysIleSerCysMetLysArgGluGluValGluAlaThrThrValVal 60
Db      483  ATGAAGCTGAGTGCAATCTCTCGCATGAAGAGGAGGAGGTGGAGGCCACCACTGTGGTG 542
Qy      61   GluTrpPheTyrArgProGluGlyGlyLysAspPheLeuIleTyrGluTyrArgAsnGly 80
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Db      783  ATACCTTTGGAGTCACTCAAGAGCGGAGAGACTTCACCTCCGTGGTCTCGGAATC 842
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Db      843  ATGATGTACATCCCTCCCTGGTCTCCTCACCTTGCTGCTGTTATTTGAGATGATCTATTGC 902
Qy      181  TyrArgLysValSerLysAlaGluGluAlaGlnGluAsnAlaSerAspTyrLeuAla 200
Db      903  TACAGAAAGTCTCTAAGCCGAGAGGCACAGAGAAATGCGTCTGACTACCTTGCT 962
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DEFINITION Rattus norvegicus mRNA for voltage-gated sodium channel beta-3
subunit.
ACCESSION AJ243395
VERSION AJ243395.2 GI:7242802
KEYWORDS scn3b gene; voltage-gated sodium channel beta-3 subunit.
SOURCE Rattus norvegicus (Norway rat)
ORGANISM Rattus norvegicus
REFERENCE
AUTHORS Morgan,K., Stevens,E.B., Shaw,B., Cox,P., Dixon,A.K., Lee,K.,
Pinnock,R.D., Higes,J., Richardson,P.J., Mizuguchi,K. and
Jackson,A.P.
TITLE beta 3: an additional auxiliary subunit of the voltage-sensitive
sodium channel that modulates channel gating with distinct kinetics
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (5), 2308-2313 (2000)
PUBMED 1068874
REFERENCE 2

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AUTHORS Morgan K.  
 TITLE Direct Submission  
 JOURNAL Submitted (28-JUN-1999) Morgan K., Biochemistry, University of Cambridge, Tennis Court Road, Cambridge, CB2 1QW, UNITED KINGDOM  
 REMARK Revised by [3]  
 REFERENCE 3 (bases 1 to 2220)  
 AUTHORS Morgan K.  
 TITLE Direct Submission  
 JOURNAL Submitted (09-MAR-2000) Morgan K., Biochemistry, University of Cambridge, Tennis Court Road, Cambridge, CB2 1QW, UNITED KINGDOM  
 COMMENT On Mar 14, 2000 this sequence version replaced gi:7161888.  
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 DEFINITION AX048005  
 ACCESSION AX048005.1 GI:11876883  
 VERSION  
 KEYWORDS  
 SOURCE Rattus sp.  
 ORGANISM Rattus sp.  
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 Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;  
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 REFERENCE  
 AUTHORS Curtis, R.A.  
 TITLE Gene encoding a sodium channel beta-3 subunit protein  
 JOURNAL Patent: WO 069912-A 22 23-NOV-2000;  
 Millennium Pharmaceuticals, Inc. (US)  
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 Pred. No.: 9,65e-115 Length: 2632  
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 QY 41 MetLysLeuArgCysIleSerCysMetLysArgGluGluValGluAlaThrThrValVal 60  
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Db 378 CAGACGCTATCCATCACTACTCAATGTCTACTTTGAATGACTCTGGCCTCTACACATGC 437
Qy 121 AsnValSerArgGluPheGluPheGluAlaHisArgProPheValLysThrArgLeu 140
Db 438 AATGTGTCAGGAGTTTGGAAATTCAGGCACACAGGCTTTTGTGAAGACACAGACTG 497
Qy 141 IleProLeuArgValThrGluGluAlaGlnGluAspPheThrSerValValSerGluIle 160
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RESULT 11
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LOCUS
DEFINITION Rattus norvegicus sodium channel beta 3 subunit (SCN3B) mRNA,
complete cds.
ACCESSION AF378093
VERSION AF378093.1 GI:14165175
KEYWORDS
SOURCE Rattus norvegicus (Norway rat)
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Rattus.
Q.Y., Curtis, R., Lawson, D., Gilbride, K., Ge, P., DiStefano P.S.,
Silos-Santiago, I., Catterall W.A. and Scheuer, T.
Differential modulation of sodium channel gating and persistent
sodium currents by the beta1, beta2, and beta3 subunits
Mol. Cell. Neurosci. 18 (5), 570-580 (2001)
11922146
PUBMED
REFERENCE 2 (bases 1 to 3107)
Curtis, R.
Direct Submission
TITLE Submitted (05-MAY-2001) Neurobiology, Millennium Pharmaceuticals
Inc., 75 Sidney Street, Cambridge, MA 02139, USA
JOURNAL Location/Qualifiers
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Pred. No.: 1105.00 Matches: 211
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Percent Similarity: 98.14% Mismatches: 4
Best Local Similarity: 98.14% Indels: 0
Query Match: 98.31% Gaps: 0
DB: 9
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Qy 81 HisGlnGluValGluSerProPheGlnGlyArgLeuGlnThrPheAsnGlySerLysAspLeu 100
Db 317 CACCAGGAAGTGGAGAGCCCTTCCAAAGGCGCTCTGCAGTGAATGGAGCAAGACCTG 376
Qy 101 GlnAspValSerIleThrValLeuAsnValThrLeuAsnAspSerGlyLeuTyrThrCys 120
Db 377 CAGACGCTATCCATCACTGCTACTCAATGTCATCTTGAATGACTCTGGCCTCTACATGC 436
Qy 121 AsnValSerArgGluPheGluPheGluAlaHisArgProPheValLysThrThrArgLeu 140
Db 437 AATGTGTCCAGGAGTTCGAATTCGAGGCACACAGGCGCTTTTGTGAAGACACAGACTG 496
Qy 141 IleProLeuArgValThrGluGluAlaGlyGluAspPheThrSerValValSerGluIle 160
Db 497 ATACCTTTGGAGTCACTGAAGAGCGGAGAGACTTCACTCCCGGGTCTCGGAATC 556
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RESULT 12
AX047984
LOCUS
DEFINITION Sequence 1 from Patent WO0069912.
ACCESSION AX047984
VERSION AX047984.1 GI:11876881
KEYWORDS
SOURCE Rattus sp.
ORGANISM Rattus sp.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Rattus.
1
Curtis, R.A.
Gene encoding a sodium channel beta-3 subunit protein
Patent: WO 0069912-A 1 23-NOV-2000;
Millennium Pharmaceuticals, Inc. (US)
Location/Qualifiers
FEATURES
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ORIGIN

Alignment Scores:  
Pred. No.: 1.56e-114 Length: 3910  
Score: 1105.00 Matches: 211  
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Best Local Similarity: 98.14% Mismatches: 4  
Query Match: 98.31% Indels: 0  
DB: 9 Gaps: 0

US-09-977-579A-2 (1-215) x BC070899 (1-3910)

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Qy 21 ValCysPheProValCysValGluValProSerGluThrGluAlaValGlnGlyAsnPro 40  
Db GTCTGTCTTCCCTGTGTGTGGAGTAGTACCTTCGGAGACAGAAAGCGGTGCGAGGGTAATCCC 497  
Qy 41 MetLysLeuArgCysIleSerCysMetLysArgGluGluValGluAlaThrValVal 60  
Db ATGAAGCTGAGTGCATCTCTCTGATGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 557  
Qy 61 GluTrpPheTyrArgProGluGlyGlyLysAspPheLeuLeuTyrGluTyrArgAsnGly 80  
Db GAGTGGTCTTACAGCGCTCAGCGCGGTAAAGATTCTCTATATATAGTAGTATCGGAATGGC 617  
Qy 81 HisGlnGluValGluSerProPheGlnGlyArgLeuGlnTrpAenGlySerLysAspLeu 100  
Db CACAGGAAGTGGAGAGCGCCCTTCAAGCGCTTCGAGTGGATGGAGGAGGAGGAGGAGGAGGAG 677  
Qy 101 GlnAspValSerIleThrValLeuAsnValThrLeuAenAspSerGlyLeuTyrThrCys 120  
Db CAGACGTATTCATCATCTGACTCTCAATGCTCACTTGAATGACTCTGGCCCTTACACATGC 737  
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Qy 141 IleProLeuArgValThrGluAlaGlyGluAspPheThrSerValValSerGluIle 160  
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Qy 181 TyrArgLysValSerLysAlaGluGluAlaGlnGluAenAlaSerAspTyrLeuAla 200  
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Qy 201 IleProSerGluAenLysGluAenSerAlaValProValGluGlu 215  
Db ATCCCTTCAGAGAACAGGAGAACTCTGTGTGTACCTGTGGAGGAA 1022

RESULT 14  
AKI73115  
LOCUS AKI73115 4025 bp mRNA linear ROD 01-MAR-2005  
DEFINITION Mus musculus mRNA for mKIAA1158 protein.  
ACCESSION AKI73115  
VERSION AKI73115.1 GI:50510814  
KEYWORDS FLI CDNA.  
SOURCE Mus musculus (house mouse)

ORGANISM

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;  
Sciurognathi; Muridae; Murinae; Mus.

REFERENCE

AUTHORS

Okazaki,N., F-Kikuno,R., Ohara,R., Inamoto,S., Koseki,H.,  
Hiraoka,S., Saga,Y., Seino,S., Nishimura,M., Kaisho,T., Hoshino,K.,  
Kitamura,H., Nagase,T., Ohara,O. and Koga,H.  
Prediction of the coding sequences of mouse homologues of KIAA  
gene: IV. The complete nucleotide sequences of screening of 500 mouse  
KIAA-homologous cDNAs identified by screening of terminal sequences  
of cDNA clones randomly sampled from size-fractionated libraries  
DNA Res. 11 (3), 205-218 (2004)

JOURNAL

PUBMED

15368995  
2 (bases 1 to 4025)  
Okazaki,N., Kikuno,R.F., Nagase,T., Ohara,O. and Koga,H.  
Direct Submission  
Submitted (19-MAY-2004) Hisashi Koga, Kazusa DNA Research  
Institute, Laboratory for Genome Informatics; 2-6-7  
Kazusa-kamatari, Kisarazu, Chiba, 292-0818, Japan  
(E-mail:mouse@kazusa.or.jp, Tel.81-438-52-3919, Fax.81-438-52-3918)  
The CREATE program supported by Japan science and technology  
corporation; cDNA full insert sequencing: Kazusa DNA Research  
Institute; cDNA library construction, clone selection and 5'- &  
3'-end one pass sequencing.

JOURNAL

COMMENT

FEATURES

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/evidence=not experimental  
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gene

CDS

ORIGIN

Alignment Scores:

Pred. No.: 1.3e-113 Length: 4025  
Score: 1097.00 Matches: 210  
Percent Similarity: 97.67% Conservativity: 0  
Best Local Similarity: 97.67% Mismatches: 5  
Query Match: 97.60% Indels: 0  
DB: 9 Gaps: 0

US-09-977-579A-2 (1-215) x AKI73115 (1-4025)

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Qy 21 ValCysPheProValCysValGluValProSerGluThrGluAlaValGlnGlyAsnPro 40  
Db GTCTGTCTTCCCTGTGTGTGTAGTAGTACCTTCGGAGACAGAAAGCGGTGCGAGGCAATTCC 409  
Qy 41 MetLysLeuArgCysIleSerCysMetLysArgGluGluValGluAlaThrThrValVal 60  
Db ATGAAGCTGAGTGCATCTCTCTGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 469



Db 428 ATGAAGCTGAGATGCAATCTCTGTCATGAAGAGGAGGAGGTGGAGGCCACCACTGTAGTG 487  
 Qy 61 GluTrpPheTyrArgProGluGlyGlyLysAspPheLeuIleTyrGluTyrArgAsnGly 80  
 Db 488 GAGTGGTTCTACAGGCTGTAGGGGGTAAAGATTTCCTTATATATGAGTATCGAAATGGC 547  
 Qy 81 HisGlnGluValGluSerProPheGlnGlyArgLeuGlnTrpAsnGlySerLysAspLeu 100  
 Db 548 CACCAGGAGGTGGAGAGCCCTTCCAGGTGCTGTCAGTGGAAATGGAGCAAGACCTG 607  
 Qy 101 GlnAspValSerIleThrValLeuAsnValThrLeuAsnAspSerGlyLeuTyrThrCys 120  
 Db 608 CAGGACGTATCCATCAGTGTCTCAATGTCACCTCTGAATGACTCTGGCCTCTACACATGT 667  
 Qy 121 AsnValSerArgGluPheGluPheGluAlaHisArgProPheValLysThrThrArgLeu 140  
 Db 668 AATGTGTCAGGGAGTTTGTAGTTCGAGCACACCGGCCCTTTGTGAAGACCACCAAGACTA 727  
 Qy 141 IleProLeuArgValThrGluGluAlaGlyGluAspPheThrSerValValSerGluIle 160  
 Db 728 ATACCCCTGCCAGTCACTGAAGAGCGGGAGAGACTTCACCTCCGTGGTCTCGGAAATC 787  
 Qy 161 MetMetTyrIleLeuLeuValPheLeuThrLeuTrpLeuLeuIleGluMetIleTyrCys 180  
 Db 788 ATGATGTACATCCTCTGGTCTTCTCCTCAGCTTGTGGCTGTTTATTGAGATGATCTATTGC 847  
 Qy 181 TyrArgLysValSerLysAlaGluGluAlaGlnGlnAlaSerAspTyrLeuAla 200  
 Db 848 TACAGAAAGGTCTCTAAGGCCGAAAGAGGAGCTCAGGAAATGGCTCTGACTACCTTGCT 907  
 Qy 201 IleProSerGluAsnLysGluAsnSerAlaValProValGluGlu 215  
 Db 908 ATCCCTTCAGAGAACAGGAGACTCTGTGTGTACCCGTGGAGGAA 952

Search completed: January 5, 2006, 17:49:40  
 Job time : 4880 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2006 Compugen Ltd.

OM protein - nucleic search, using frame\_plus\_p2n model  
Run on: January 5, 2006, 18:20:53 ; Search time 587 Seconds  
(without alignments)  
2441.071 Million cell updates/sec

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Perfect score: 1124  
Sequence: 1 MPATNRLPPLASLVIYWS.....SDYLAIPTSENKENSAPVPEE 215

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Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 4996997 seqs, 3332346308 residues  
Total number of hits satisfying chosen parameters: 9993994

Minimum DB seq length: 0  
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Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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12: geneseqm2004as.\*  
13: geneseqm2004bs.\*  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1124	100.0	1261	3 AAC67837	Aac67837 Human bet
2	1124	100.0	1261	10 ADB78651	Adb78651 Human ion
3	1124	100.0	1261	10 ACF57870	Acf57870 Human SCN
4	1124	100.0	1510	4 AAF84146	Aaf84146 Human nov

5	1124	100.0	4052	6 ABA93727	Aba93727 Human eig
6	1105	98.3	645	5 AAC90601	Aac90601 Rat sodiu
7	1105	98.3	2220	3 AAC67836	Aac67836 Rat beta3
8	1105	98.3	2632	5 AAC90602	Aac90602 Rat sodiu
9	1105	98.3	3108	5 AAC90600	Aac90600 Rat sodiu
10	1024	91.1	1045	4 AAK52345	Aak52345 Human pol
11	1003	89.2	978	4 AAH98320	Aah98320 Human EST
12	1003	89.2	978	13 ADS11487	Ads11487 Human the
13	97.5	82.5	1195	5 AAS86764	Aas86764 DNA encod
14	86.5	78.9	953	13 ADS10151	Ads10151 Human the
15	742	66.0	471	2 AAV86895	Aav86895 EST clone
16	694	61.7	3531	5 AAS86763	Aas86763 DNA encod
17	477	42.4	657	5 AAC90603	Aac90603 Rabbit so
18	473	42.1	1335	10 ACF57868	Acf57868 Human SCN
19	473	42.1	1335	12 ADQ19428	Adq19428 Human sof
20	473	42.1	1414	8 ABZ23837	Abz23837 Human vol
21	473	42.1	1414	14 ADY27074	Ady27074 Human SCN
22	472	42.0	1414	10 ADB78640	Adb78640 Human ion
23	472	42.0	1490	6 ABK63747	Abk63747 Rat sequ
24	472	42.0	1490	10 ADB52855	Adb52855 Primary r
25	472	42.0	1490	12 ADO09498	Ado09498 Rat sodiu
26	472	42.0	1490	13 ADV41127	Adv41127 Rat card
27	471	41.9	657	14 ADV42849	Adv42849 Human psy
28	465	41.4	1414	10 ADB78641	Adb78641 Human ion
29	408.5	36.3	621	5 AAS86762	Aas86762 DNA encod
30	262.5	23.4	850	4 AAF57675	Aaf57675 Rat sodiu
31	262.5	23.4	850	4 AAF30669	Aaf30669 Sodium ch
32	260.5	23.2	974	6 AAD29622	Aad29622 Human bet
33	234	20.8	407	4 ABA08942	Aba08942 Human vol
34	234	20.8	407	4 AAK53329	Aak53329 Human pol
35	230	20.5	855	10 ADG15041	Adg15041 Human SEC
36	218.5	19.4	358	10 ACD98234	Acd98234 Human col
37	172	15.3	747	14 AEA46527	Aea46527 Mouse mye
38	167	14.9	1029	9 ACF25382	Acf25382 Rat schwa
39	165.5	14.7	3583	12 ADQ23651	Adq23651 Human sof
40	163.5	14.5	777	6 ABA02395	Aba02395 Human mye
41	163.5	14.5	1693	12 ADF45442	Adf45442 Human vas
42	161.5	14.4	162	12 ADM66944	Adm66944 Human adi
43	160.5	14.3	970	4 AAF27741	Aaf27741 Human tra
44	160.5	14.3	983	4 AAD02925	Aad02925 Human PRO
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ALIGNMENTS

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AC AAC67837;  
XX  
DT 15-FEB-2001 (first entry)  
XX  
DE Human beta3 cDNA.  
XX  
KW Human; beta sub-unit; beta3; analgesic; anticonvulsant;  
KW cerebroprotective; vasotropic; cardiant; nootropic; cytostatic;  
KW dermatological; gene therapy; voltage-gated sodium channel; pain;  
KW epilepsy; stroke; ischaemia; heart disease; Jacobean Syndrome;  
KW familial nonchromaffin paraganglioma; phenylketonuria;  
KW Charcot Marie Tooth disease; ss.  
XX Homo sapiens.  
XX  
XX WO200063367-A1.  
XX  
XX 26-OCT-2000.  
XX  
XX 24-FEB-2000; 2000WO-EP001783.  
XX  
XX 15-APR-1999; 99US-0129473P.  
PA (WARN ) WARNER LAMBERT CO.

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PA (UYCA-) UNIV CAMBRIDGE TECH SERVICES LTD.
XX
PI Cox P, Dixon A, Jackson A, Morgan K;
XX
DR WPI; 2000-665241/64.
XX
DR P-PSDB; AAB36002.
XX
PT Novel nucleic acids encoding a beta-3 subunit from a voltage-gated sodium
PT channel, and their corresponding polypeptides, useful for detecting and
PT treating sodium channel-associated conditions, e.g. pain, epilepsy and
PT stroke.
XX
XX Claim 10; Page 70-71; 88pp; English.
XX
XX The present sequence is given in the claims of a specification relating
CC to a novel family of beta sub-unit proteins from a voltage-gated sodium
CC channel. Human and rat beta sub-units, which have been collectively
CC identified as beta3, have been isolated. The polynucleotides and
CC polypeptides are useful for screening for agonists and antagonists of
CC sodium channels. The agonists, antagonists, proteins and nucleic acids
CC may be used diagnosing of treating diseases or conditions associated with
CC voltage-gated sodium channels, e.g. pain, epilepsy, stroke, ischaemia,
CC heart disease, Jacobsen Syndrome, Familial Nonchromaffin Paraganglioma,
CC Phenylketonuria and Charcot Marie Tooth disease
XX
SQ Sequence 1261 BP; 263 A; 366 C; 372 G; 260 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 2.66e-124 Length: 1261
Score: 1124.00 Matches: 215
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 3 Gaps: 0

US-09-977-579A-2 (1-215) x AAC67837 (1-1261)

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Db 436 GTCTGCTTCCCTGTGTGTGGAGTGCCTTCGGAGACGGAGCGCGTGCAGGGCAACCCC 495
Qy 41 MetLysLeuArgCysIleSerCysMetLysArgGluGluValGluAlaThrValVal 60
Db 496 ATGAAGCTGCCCTGCATCTCTCGCATGAAGAGAGAGAGGGTGGAGGCCACCACCGTGGTG 555
Qy 61 GluTrpPheTyrArgProGluGlyCysLysAspPheLeuIleTyrGluTyrArgAsnGly 80
Db 556 GAATGGTGTCTACAGGCCCGAGGGCGGTAAGATTTCCTTATTTACGAGTATCGGAATGGC 615
Qy 81 HisGlnGluValGluSerProPheGlnGlyArgLeuGlnTrpAsnGlySerLysAspLeu 100
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Qy 101 GlnAspValSerIleThrValLeuAsnValThrLeuAsnAspSerGlyLeuTyrThrCys 120
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Qy 141 IleProLeuArgValThrGluGluAlaGlyGluAspPheThrSerValValSerGluIle 160
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Db 976 ATCCCATCTGAGAACACAGGAGACTCTGCGGTACCACTGGAGGAA 1020

RESULT 2
ADB78651
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XX
AC ADB78651;
XX
XX 04-DEC-2003 (first entry)
XX
DE Human ion channel subunit cDNA mutant SCN1AR exon 1 SEQ ID NO:22.
XX
KW ss; gene; mutant; ion channel; ion channel subunit; ICS; nootropic;
KW neuroprotective; inotropic; antipyrretic; antiarrhythmic; antimigraine;
KW antidepressant; antiparkinsonian; neuroleptic; tranquiliser; analgesic;
KW nephrotropic; antidiabetic; ophthalmological; epilepsy;
KW ion channel dysfunction; human.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN WO2003008574-A1.
XX
PD 30-JAN-2003.
XX
PF 08-JUL-2002; 2002WO-AU000910.
XX
PR 18-JUL-2001; 2001AU-00006452.
PR 05-MAR-2002; 2002AU-00000910.
PR 13-MAY-2002; 2002AU-00002292.
XX
XX (BION-) BIONOMICS LTD.
PA (WALL/) WALLACE R W.
XX
PI Mulley JC, Harkin LA, Dibbens LM, Phillips HA, Heron SE;
XX
XX Berkovic SP, Scheffer IE;
XX
XX WPI; 2003-239332/23.
XX
PT Identifying predisposition to an ion channel dysfunction, such as
PT periodic paralysis, cardiac arrhythmias, migraine, Alzheimer's disease,
PT schizophrenia, anxiety and depression, by detecting encoding-gene
PT mutation events.
XX
PS Claim 6; SEQ ID NO 22; 106pp; English.
XX
CC The invention relates to a novel method for identifying a subject
CC predisposed to a disorder associated with ion channel dysfunction. The
CC method comprises ascertaining if at least one of the genes encoding ion
CC channel subunits (ICS) has undergone a mutation event so that a cDNA
CC derived from the subject has any of 134 nucleotide sequences. The method
CC of the invention has nootropic, neuroprotective, inotropic, antipyrretic,
CC antiarrhythmic, antimigraine, antidepressant, antiparkinsonian,
CC neuroleptic, tranquiliser, analgesic, nephrotropic, antidiabetic, and
CC ophthalmological activity. A polynucleotide of the invention acts as an
CC ion channel agonist, or ion channel antagonist. The methods, isolated
CC nucleic acids, polypeptides, antibody, selective agonist, antagonist or
CC modulator of an ion channel, cells and genetically modified non-human
CC animal, are useful for the diagnosis and treatment of epilepsy and/or a
CC disorder associated with ion channel dysfunction, such as hyper- or hypo-
CC kalemic periodic paralysis, myotonias, malignant hyperthermia,
CC myasthenia, cardiac arrhythmias, episodic ataxia, migraine, Alzheimer's
CC disease, Parkinson's disease, schizophrenia, hyperkplexia, anxiety,
CC depression, phobic obsessive symptoms, neuropathic pain, inflammatory
CC pain, chronic/acute pain, Bartter's syndrome, polycystic kidney disease,
CC Dent's disease, hyperinsulinaemic hypoglycaemia of infancy, cystic
CC fibrosis, congenital stationary night blindness and total colour
```

CC blindness. The present sequence represents a mutant cDNA of the  
CC invention. The sequence data for this patent is not represented in the  
CC printed specification, but was obtained in electronic format directly  
CC from WIPO at ftp.wipo.int/pub/published\_pat\_sequences.

XX SQ Sequence 1261 BP; 263 A; 365 C; 372 G; 261 T; 0 U; 0 Other;

Alignment Scores:  
Pred. No.: 2.66e-124 Length: 1261  
Score: 1124.00 Matches: 215  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 10 Gaps:

US-09-977-579A-2 (1-215) x ADB78651 (1-1261)

QY 1 MetProAlaPheAsnArgLeuPheProLeuAlaSerLeuValLeuIleTyrTrpValSer 20  
DB 376 ATGCTTGCTTCAATAGATTGTTCCCTGGCTTCTCGTGTATCTACTGGTCACT 435  
QY 21 ValCysPheProValCysValGluValProSerGluThrGluAlaValGlnGlyAsnPro 40  
DB 436 GTCTGCTTCCCTGTGTGTGAAGTGCCTCGAGACGGAGCGGTGAGGCAACCCC 495  
QY 41 MetLysLeuArgCysIleSerCysMetLysArgGluGluValGluAlaThrThrValVal 60  
DB 496 ATGAAGCTGCGTGCATCTCTCCATGATGAAGAGAGAGAGGTGGAGCCACACGGTGGT 555  
QY 61 GluTrpPheTyrArgProGluGlyGlyLysAspPheLeuIleTyrGluTyrArgAsnGly 80  
DB 556 GAATGGTCTACAGGCCCGAGCGCGTAAAGATTTCCTTATTACGATATCGGAATGCG 615  
QY 81 HisGlnGluValGluSerProPheGlnGlyArgLeuGlnTrpAsnGlySerLysAspLeu 100  
DB 616 CACCAAGAGGTGAGAGGCCCTTTACAGGCGCTGAGTGAATGGCAGCAAGACCTG 675  
QY 101 GlnAspValSerIleThrValLeuAsnValThrLeuAsnAspSerGlyLeuTyrThrCys 120  
DB 676 CAGGACGTGTCCATCACTGTGCTCAACGTCATCTGAACGACTCTGGCCCTTACACCTGC 735  
QY 121 AsnValSerArgGluPheGluPheGluAlaHisArgProPheValLysThrThrArgLeu 140  
DB 736 ATGTGTCCCGGAGTTTGTGAGGCGCATCGGCCCTTTGTGAAGACGACGCGGTG 795  
QY 141 IleProLeuArgValThrGluGluAlaGlyGluAspPheThrSerValValSerGluIle 160  
DB 796 ATCCCCCTTAAGAGTCACTCAGGAGGCTGGAGAGGACTTCACCTCTGTGTGCTCAGAAATC 855  
QY 161 MetMetTyrIleLeuLeuValPheLeuThrLeuThrLeuIleGluMetIleTyrCys 180  
DB 856 ATGATGTACATCTCTGCTTCTCTCCTCACCCCTGTGGCTCTCATCGAGATGATATTGC 915  
QY 181 TyrArgLysValSerLysAlaGluGluAlaAlaGlnGluAsnAlaSerAspTyrLeuAla 200  
DB 916 TACAGAAAGGTCTCAAAAGCCGAGAGGAGGAGCCCAAGAAACCGCTCTGACTACCTTGC 975  
QY 201 IleProSerGluAsnLysGluAsnSerAlaValProValGluGlu 215  
DB 976 ATCCCATCTGAGAACAAAGAGAACTCTCGCGGTACCACTGAGGAGAA 1020

## RESULT 3

ACF57870

ID ACF57870 standard; cDNA; 1261 BP.

XX AC

AC ACF57870;

XX XX

DT 15-JAN-2004 (first entry)

XX XX

DE Human SCN3B protein encoding cDNA.

DE XX

KW SCN1A; sodium channel type 1 alpha-subunit; anticonvulsant; analgesic;  
neuroprotective; anesthetic; cytostatic; cerebroprotective; cardiant;

KW hypotensive; gene therapy; SCN3B; human; gene; ss.

XX OS

XX Homo sapiens.

XX Key

FT CDS Location/Qualifiers

FT 376..1023

FT /\*tag= a

FT /product= "SCN3B"

XX WO2003072751-A2.

XX PN

XX 04-SEP-2003.

XX PD

XX 25-FEB-2003; 2003WO-US006010.

XX PF

XX 25-FEB-2002; 2002US-0359382P.

XX PA (UYVA-) UNIV VANDERBILT.

XX George AL, Lossin C;

XX WPI; 2003-712725/67.

XX P-FSDB; ABR83183.

XX DR

XX Recombinantly expressed sodium channel type 1 alpha subunit, useful in

XX screening for modulators, for treating e.g. epilepsy.

XX PS Disclosure; Page 145-147; 176pp; English.

XX CC

CC The invention relates to a recombinantly expressed and isolated human

CC SCN1A (sodium channel type 1 alpha-subunit) (I). (I), optionally

CC incorporated into a cell, is used to screen for specific modulators,

CC potentially useful as anticonvulsant, antiepileptic, neuroprotective,

CC analgesic and/or anesthetic agents, e.g. for treating severe myoclonic

CC epilepsy of infancy, stroke, cardiac arrest, hyperkalemic paralysis,

CC motor endplate diseases, hypertension, congestive heart failure and

CC muscular dystrophy also to treat cancer (SCN1A is expressed in prostatic

CC and metastatic cancer cell lines). These activities can also be provided

CC by gene therapy vectors that express (I) or the modulators. The

CC modulators, also antibodies directed against (I), are used to detect

CC sodium channel polypeptides. The present sequence represents a human

CC SCN3B protein encoding cDNA

XX SQ

Sequence 1261 BP; 263 A; 365 C; 372 G; 260 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 2.66e-124 Length: 1261

Score: 1124.00 Matches: 215

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 100.00% Indels: 0

DB: 10 Gaps:

US-09-977-579A-2 (1-215) x ACF57870 (1-1261)

QY 1 MetProAlaPheAsnArgLeuPheProLeuAlaSerLeuValLeuIleTyrTrpValSer 20

DB 376 ATGCTTGCTTCAATAGATTGTTCCCTGGCTTCTCGTGTATCTACTGGTCACT 435

QY 21 ValCysPheProValCysValGluValProSerGluThrGluAlaValGlnGlyAsnPro 40

DB 436 GTCTGCTTCCCTGTGTGTGAAGTGCCTCGAGACGGAGCGGTGAGGCAACCCC 495

QY 41 MetLysLeuArgCysIleSerCysMetLysArgGluGluValGluAlaThrThrValVal 60

DB 496 ATGAAGCTGCGTGCATCTCTCCATGATGAAGAGAGAGAGGTGGAGCCACACGGTGGT 555

QY 61 GluTrpPheTyrArgProGluGlyGlyLysAspPheLeuIleTyrGluTyrArgAsnGly 80

DB 556 GAATGGTCTACAGGCCCGAGCGCGTAAAGATTTCCTTATTACGATATCGGAATGCG 615

QY 81 HisGlnGluValGluSerProPheGlnGlyArgLeuGlnTrpAsnGlySerLysAspLeu 100



```
Db 616 CACCAGAGGTGGAGAGCCCTTTTCAGGGGCGCTGCGAGTGAATGGCAAGGACCTG 675
Qy 101 GlnAspValSerIleThrValLeuAsnValThrLeuAsnAspSerglyLeuTyrThrCys 120
Db 676 CAGGACGTGTCCATCACTGTGCTCAACGTCACTCTGAACGACTCTGGCCTCTACACCTGC 735
Qy 121 AsnValSerArgGluPheGluAlaHisArgProPheValIysThrArgLeu 140
Db 736 AATGTGTCCTCCGGAGTTTGAGTTTGAGCGCATCGGCCCTTTGTGAAGACACGCGCTG 795
Qy 141 IleProLeuArgValThrGluAlaGlyLeuAspPheThrSerValValSerGluIle 160
Db 796 ATCCCTTAAGATCACCAGAGGCTGGAGAGACTTCACCTCTGTGGTCTCAGAAATC 855
Qy 161 MetMetTyrIleLeuLeuValPheLeuThrLeuTrpLeuIleGluMetIleTyrCys 180
Db 856 ATGATGTACATCTCTGCTCTCCTCACCTGCTGGCTGCTCATCGAGATGATATATGC 915
Qy 181 TyrArgIysValSerIysAlaGluAlaGlyLeuAlaGlnGluAsnAlaSerAspTyrLeuAla 200
Db 916 TACAGAAAGGTCTCAAAAGCCGAAAGAGCAGCCCAAGAAACGCGTCTGTACTACCTTGCC 975
Qy 201 IleProSerGluAsnLysGluAsnSerAlaValProValGluGlu 215
Db 976 ATCCCATCTGAGACAGGAGAACTCTGCGGTACCACTGGAGGAA 1020

RESULT 4
AAF84146
ID AAF84146 standard; cDNA; 1510 BP.
XX
AC AAF84146;
XX
XX 07-SEP-2001 (first entry)
XX
DE Human novel sodium channel betal-like subunit encoding cDNA.
XX
KW Sodium channel; sensory neurone specific channel; betal-like subunit;
KW SNS; therapeutic; pain; analgesic; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT 213..860
FT /*tag= a
FT /product= "sodium channel betal-like subunit"
XX
XX WO200144293-A2.
XX
XX 21-JUN-2001.
XX
XX 14-DEC-2000; 2000WO-GB004802.
XX
XX P-PSDB; AAB85206.
XX
XX 17-DEC-1999; 99GB-00029970.
XX
XX (GLAX ) GLAXO GROUP LTD.
XX
XX Plumpton M, Powell AJ, Sanseau P;
XX
XX WPI; 2001-398129/42.
XX
XX P-PSDB; AAB85206.
XX
XX
XX Novel sub-unit for voltage-gated sodium channel proteins for producing
XX agents useful for treating pain.
XX
XX
XX Claim 4; Page 29-30; 31pp; English.
XX
XX The invention provides a novel betal-like sub-unit for voltage-gated
XX sodium ion channel polypeptide, specifically a sensory neurone specific
XX channel (SNS) subunit. The novel betal-like subunit is useful for
XX producing a therapeutic agent which is useful treating pain in a patient.
XX The subunit can be expressed by standard recombinant methodology. The
XX present sequence represents a human novel sodium channel betal-like
XX subunit encoding cDNA
```

```
XX SQ Sequence 1510 BP; 350 A; 410 C; 414 G; 336 T; 0 U; 0 Other;
Alignment Scores:
Pred. No.: 3.43e-124 Length: 1510
Score: 1124.00 Matches: 215
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0
US-09-977-579A-2 (1-215) x AAF84146 (1-1510)
Qy 1 MetProAlaPheAsnArgLeuPheProLeuAlaSerLeuValLeuIleTyrTrpValSer 20
Db 213 ATGCCTCCCTTCAATAGATTGTTTCCCTCGCTTCTCTCGTGTATCTACTCTGGTCACT 272
Qy 21 ValCysPheProValCysValGluValProSerGluThrGluAlaValGlnGlyAsnPro 40
Db 273 GTCTGCTTCCCTGTGTGTGTGGAAAGTCCCTCGGAGACGAGGCCGTGCAGGGCAACCCC 332
Qy 41 MetIysLeuArgCysIleSerCysMetIysArgGluGluValGluAlaThrThrValVal 60
Db 333 ATGAAGCTGCGCTGCATCTCTGCATGAAGAGAGAGAGGTGGAGGCCACCACCGTGGTG 392
Qy 61 GluTrpPheTyrArgProGluGlyGlyIysAspPheLeuIleTyrGluTyrArgAsnGly 80
Db 393 GAATGGTTTCTACAGGCCCGGCGGTAAAGATTCTCTTATTTACGAGTATCGGAATGGC 452
Qy 81 HisGlnGluValGluSerProPheGlnGlyArgLeuGlnTrpAsnGlySerLysAspLeu 100
Db 453 CACCAGAGGTGGAGAGCCCTTTTCAGGGGCGCTGCGATGGAAATGGCAGACGACCTG 512
Qy 101 GlnAspValSerIleThrValLeuAsnValThrLeuAsnAspSerglyLeuTyrThrCys 120
Db 513 CAGGACGTGTCCATCACTGTGCTCAACGTCACTCTGAACGACTCTGGCCTCTACACCTGC 572
Qy 121 AsnValSerArgGluPheGluAlaHisArgProPheValIysThrThrArgLeu 140
Db 573 AATGTGTCCTCCGGAGTTTGAGTTTGAGCGCATCGGCCCTTTGTGAAGACACGCGCTG 632
Qy 141 IleProLeuArgValThrGluGluAlaGlyLeuAspPheThrSerValValSerGluIle 160
Db 633 ATCCCCCTAAGATCACCAGAGGCTGGAGAGACTTCACCTCTGTGGTCTCAGAAATC 692
Qy 161 MetMetTyrIleLeuLeuValPheLeuThrLeuTrpLeuIleGluMetIleTyrCys 180
Db 693 ATGATGTACATCTCTGCTCTCTCCTCACCTTGTGGCTGCTCATCGAGATGATATATGC 752
Qy 181 TyrArgIysValSerIysAlaGluAlaGlnGluAsnAlaSerAspTyrLeuAla 200
Db 753 TACAGAAAGGTCTCAAAAGCCGAAAGAGCAGCCCAAGAAACGCGTCTGTACTACCTTGCC 812
Qy 201 IleProSerGluAsnLysGluAsnSerAlaValProValGluGlu 215
Db 813 ATCCCATCTGAGACAGGAGAACTCTGCGGTACCACTGGAGGAA 857

RESULT 5
ABA93727
ID ABA93727 standard; cDNA; 4052 BP.
XX
XX ABA93727;
XX
XX 30-APR-2002 (first entry)
XX
XX Human signal transduction cDNA clone amy2_2f18.
XX
XX Human; foetal brain; foetal kidney; melanoma; testis; amygdala;
XX gene therapy; ss.
XX
XX Homo sapiens.
XX
XX WO200198454-A2.
XX
```

XX PD 27-DEC-2001.  
XX PF 25-APR-2001; 2001WO-IB002050.  
XX PR 25-APR-2000; 2000US-0199380P.  
XX XX (GEHU-) GERMAN HUMAN GENOME PROJECT.  
XX PA Wiemann S;  
XX DR WPI; 2002-055860/07.  
XX DR P-PSDB; ABB05689.  
XX PT Human cDNA sequences and clones derived from human fetal brain, fetal  
PT kidney, melanoma, testis and amygdala cDNA libraries, useful in genetic  
PT screening and therapy.  
XX PS Claim 1; Page 174-175; 611pp; English.  
XX CC The present invention describes assemblies and computer readable media  
CC comprising novel human cDNA sequences and clones derived from human  
CC foetal brain, foetal kidney, melanoma, testis and amygdala cDNA  
CC libraries. ABA93702 to ABA93766 represent human cDNA sequences from the  
CC present invention which encode the proteins given in ABB05662 to  
CC ABB05729. The human cDNA sequences and clones can be used in gene  
CC therapy. The clones may be used in a variety of applications, for example  
CC they may be used in profiling assays, for providing large arrays of human  
CC genetic material for implementing large-scale screening strategies and  
CC for treating diseases via gene therapy procedures  
XX SQ Sequence 4052 BP; 994 A; 1033 C; 1036 G; 989 T; 0 U; 0 Other;

Alignment Scores:  
Pred. No.: 1.4e-123 Length: 4052  
Score: 1124.00 Matches: 215  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 6 Gaps: 0

US-09-977-579A-2 (1-215) x ABA93727 (1-4052)

QY 1 MetProAlaPheAsnArgLeuPheProLeuAlaSerLeuValLeuIleTyrTrpValSer 20  
DB 804 ATGCCTGCCTTCAATAGATTGTTCCCTGGCTTCTCTGCTTATCTACTGGGTCAGT 863  
QY 21 ValCysPheProValCysValGluValProSerGluThrGluAlaValGlnGlyAsnPro 40  
DB 864 GTCTGCTTCCCTGTGTGTGGAGTGCCTCGAGACGGAGCCGTGCAGGCCAACCC 923  
QY 41 MetLysLeuArgCysIleSerCysMetLysArgGluGluValGluAlaThrValVal 60  
DB 924 ATGAAGCTGGCTGCATCTCTCATGAAGAGAGAGAGGTGGAGGCCACCAACGGTGGTG 983  
QY 61 GluTrpPheTyrArgProGluGluGlyLysAspPheIleTyrGluTyrArgAsnGly 80  
DB 984 GAATGGTTCTACAGGCCCGGCGGTAAAGATTCTCTTATTACAGGATATCGAATGCC 1043  
QY 81 HisGlnGluValGluSerProPheGlnGlyArgLeuGlnTyrAsnGlySerLysAspLeu 100  
DB 1044 CACAGAGGTGGAGAGCCCTTTTCAGGGCGCCTCGAGTGGAGTGGCAGCAGGACCTG 1103  
QY 101 GlnAspValSerIleThrValLeuAsnValThrLeuAsnAspSerGlyLeuTyrThrCys 120  
DB 1104 CAGAGCGTGCATCTACTGTGCTCAAGCTCACTCTGAACGACTCTGGCCTCTACACTGC 1163  
QY 121 AsnValSerArgGluPheGluPheGluAlaHisArgProPheValLysThrThrArgLeu 140  
DB 1164 AATGTGTCCCGGAGTTTGAAGTTTGAGGGCGCATCGGCCCTTTGTGAAGACGACGGCGTG 1223  
QY 141 IleProLeuArgValThrGluGluAlaGlyLysAspPheThrSerValValSerGluIle 160

DB 1224 ATCCCCCTAAGATCACCAGGAGGCTGGAGAGACTTACCTCTGTGGTCTCAGAAATC 1283  
QY 161 MetMetTyrIleLeuLeuValPheLeuThrLeuTyrLeuIleGluMetIleTyrCys 180  
DB 1284 ATGATGTACATCCTTCTGGTCTTCTACCTTGTGGCTGCTCATCGAGATGATATATTC 1343  
QY 181 TyrArgLysValSerLysAlaGluGluAlaGlnGluAsnAlaSerAspTyrLeuAla 200  
DB 1344 TACAGAAAGGTCTCAAAAGCCGAGAGGAGCCCAAGAAACGCGTCTGACTACCTTGCC 1403  
QY 201 IleProSerGluAsnLysGluAsnSerAlaValProValGluGlu 215  
DB 1404 ATCCCATCTGAGAACAGGAGAACTCTCGGTACCAGTGGAGGAA 1448

#### RESULT 6

AAC90601

ID AAC90601 standard; cDNA; 645 BP.

XX AC AAC90601;

XX DT 13-MAR-2001 (first entry)

XX DE Rat sodium channel beta3 protein Alrxa94h5 partial coding sequence.

XX KW Rat; sodium channel beta3 protein; Alrxa94h5; pain; sleep disorder;

XX KW neurodegenerative disorder; mood disorder; muscle contraction; ss.

XX OS Rattus sp.

XX PN WO200069912-A1.

XX PD 23-NOV-2000.

XX PF 12-MAY-2000; 2000WO-US013144.

XX PR 14-MAY-1999; 99US-0134198P.

XX PA (MILL-) MILLENNIUM PHARM INC.

XX PI Curtis RAJ;

XX DR WPI; 2001-122743/13.

PT New rat sodium channel beta-3 subunit gene isolated from a rat dorsal  
PT root ganglion cDNA library for use in chromosome mapping, forensic  
PT medicine, monitoring clinical trials and therapeutics.  
XX Claim 1; Page 40-41; 145pp; English.  
XX The present invention provides the protein and coding sequences of the  
XX rat sodium channel beta3 protein, designated Alrxa94h5. This protein is  
XX involved in the generation of pain and other sensory or perceptible nerve  
XX impulses, in the establishment and endurance of mood, neurodegenerative  
XX and sleep disorders, and in the control of muscle contraction, including  
XX movements such as the heartbeat, digestion and vascular tone. The  
XX sequences can be used in predictive medicine, screening and diagnostic  
XX assays, and in pharmacogenomics  
XX SQ Sequence 645 BP; 155 A; 154 C; 181 G; 155 T; 0 U; 0 Other;

#### Alignment Scores:

Pred. No.: 1.93e-122 Length: 645  
Score: 1105.00 Matches: 211  
Percent Similarity: 98.14% Conservative: 0  
Best Local Similarity: 98.14% Mismatches: 4  
Query Match: 98.31% Indels: 0  
DB: 5 Gaps: 0

US-09-977-579A-2 (1-215) x AAC90601 (1-645)

QY 1 MetProAlaPheAsnArgLeuPheProLeuAlaSerLeuValLeuIleTyrTrpValSer 20  
DB 1 ATGCCTGCCTTCAACAGATTGCTTCCCTAGCTTCTTAGTGTCTACTACTGGGTGAGA 60

QY 21 ValCysPheProValCysValGluValProSerGluThrGluAlaValGlnGlyAsnPro 40  
 DB 61 GTCTGCTTCCCTGTGTGTGGAGTGCCTCGAGACAGAAAGCGGTGCGAGGCAATCCC 120  
 QY 41 MetLysLeuArgCysIleSerCysMetLysArgGluGluValGluAlaThrThrValVal 60  
 DB 121 ATGAAGCTGAGTGCATCTCTGTCATGAGAGGAGGAGGTGGAGGCCACCATGTGGTG 180  
 QY 61 GluTrpPheTyrArgProGluGlyGlyAspPheLeuIleTyrGluTyrArgAsnGly 80  
 DB 181 GAGTGGTTCACAGGCTTACAGGCGTAAAGATTTCTTATATAGATTCGGAATGCG 240  
 QY 81 HisGlnGluValGluSerProPheGlnClyArgLeuGlnTTPAsnGlySerLysAspLeu 100  
 DB 241 CACAGGAGTGGAGAGCCCTTCCAAAGGCCGTCTGCAGTGGATGGAGCAAGACCTG 300  
 QY 101 GlnAspValSerIleThrValLeuAsnValThrLeuAsnAspSerGlyLeuTyrThrCys 120  
 DB 301 CAGACGTATCCATCACTGACTCAATGTCACTTTGAATGACTCTGGCCTCACATGC 360  
 QY 121 AsnValSerArgGluPheGluPheGluAlaHisArgProPheValLysThrThrArgLeu 140  
 DB 361 AATGTGTCAGGAGTTCGAATTCGAGGCACACAGGCCCTTTGTGAAGACCACGAGACTG 420  
 QY 141 IleProLeuArgValThrGluGluAlaGlyGluAspPheThrSerValValSerGluIle 160  
 DB 421 ATACCTTTGCGAGTCACTGAAGAGCGGAGAGACTTCACCTCCGGTGTCTCGGAATC 480  
 QY 161 MetMetTyrIleLeuLeuValPheLeuThrLeuTyrLeuIleGluMetIleTyrCys 180  
 DB 481 ATGATGTACATCTCTCTGCTTCTCACCTGTGGCTGTTATTTAGATGATCTATTGC 540  
 QY 181 TyrArgLysValSerLysAlaGluGluAlaGlnGlnAlaGlnGlnAlaSerAspTyrLeuAla 200  
 DB 541 TACAGAAAGGTCTCTAAGGCCGAGAGAGGACAGCAGAGGAAATGCGTCTGACTACTTGTCT 600  
 QY 201 IleProSerGluAsnLysGluAsnSerAlaValProValGluGlu 215  
 DB 601 ATCCCTTCAGAGAACAGGAGACTCTGTGTGTACCTGTGGAGGAA 645

RESULT 7

ID AAC67836 standard; cDNA; 2220 BP.  
 XX  
 AC AAC67836;  
 XX  
 DT 15-FEB-2001 (first entry)  
 XX  
 DE Rat beta3 subunit cDNA.  
 XX  
 KW Rat; beta sub-unit; beta3; analgesic; anticonvulsant; cerebroprotective;  
 KW vasotrophic; cardiant; nootropic; cytostatic; dermatological;  
 KW gene therapy; voltage-gated sodium channel; pain; epilepsy; stroke;  
 KW ischaemia; heart disease; Jacobsen Syndrome;  
 KW familial nonchromaffin paraganglioma; phenylketonuria;  
 KW Charcot Marie Tooth disease; ss.  
 XX  
 OS Rattus sp.  
 XX  
 PN W0200063367-Al.  
 XX  
 PD 26-OCT-2000.  
 XX  
 XX 24-FEB-2000; 2000WO-EP001783.  
 XX  
 XX 15-APR-1999; 99US-0129473P.  
 XX  
 XX (WARN ) WARNER LAMBERT CO.  
 XX (UYCA-) UNIV CAMBRIDGE TECH SERVICES LTD.  
 XX  
 XX Cox P, Dixon A, Jackson A, Morgan K;  
 XX  
 XX

DR WPI; 2000-665241/64.  
 DR P-PSDB; AAB36001.

XX Novel nucleic acids encoding a beta-3 subunit from a voltage-gated sodium channel, and their corresponding polypeptides, useful for detecting and treating sodium channel-associated conditions, e.g. pain, epilepsy and stroke.

XX Claim 6; Page 69-70; 88pp; English.

XX The present sequence is given in the claims of a specification relating to a novel family of beta sub-unit proteins from a voltage-gated sodium channel. Human and rat beta sub-units, which have been collectively identified as beta3, have been isolated. The polynucleotides and polypeptides are useful for screening for agonists and antagonists of sodium channels. The agonists, antagonists, proteins and nucleic acids may be used diagnosing of treating diseases or conditions associated with voltage-gated sodium channels, e.g. pain, epilepsy, stroke, ischaemia, heart disease, Jacobsen Syndrome, Familial Nonchromaffin Paraganglioma, Phenylketonuria and Charcot Marie Tooth disease

XX Sequence 2220 BP; 573 A; 557 C; 561 G; 529 T; 0 U; 0 Other;

Alignment Scores:  
 Pred. No.: 1.12e-121 Length: 2220  
 Score: 1105.00 Matches: 211  
 Percent Similarity: 98.14% Conservatives: 0  
 Best Local Similarity: 98.14% Mismatches: 4  
 Query Match: 98.31% Indels: 0  
 DB: 3 Gaps: 0

US-09-977-579A-2 (1-215) x AAC67836 (1-2220)

QY 1 MetProAlaPheAsnArgLeuPheProLeuAlaSerLeuValLeuIleTyrTrpValSer 20  
 DB 363 ATGCCTCCCTTCAACAGATTGCTTCCCTAGCTTCTCTAGTGTCTATCTAGTGGTCTGAGA 422  
 QY 21 ValCysPheProValCysValGluValProSerGluThrGluAlaValGlnGlyAsnPro 40  
 DB 423 GTCTGCTTCCCTGTGTGTGGAGTGCCTTCGAGACAGAGCGGTGCGAGGCAATCCC 482  
 QY 41 MetLysLeuArgCysIleSerCysMetLysArgGluGluValGluAlaThrThrValVal 60  
 DB 483 ATGAAGCTGAGTGCATCTCTGTCATGAAGAGGAGGAGGTGGAGGCCACCATGTGGTG 542  
 QY 61 GluTrpPheTyrArgProGluGlyGlyAspPheLeuIleTyrGluTyrArgAsnGly 80  
 DB 543 GAGTGGTTCACAGGCCCTGAGGCGGTAAAGATTTCTTATATAGATTCGGAATGGC 602  
 QY 81 HisGlnGluValGluSerProPheGlnGlyArgLeuGlnTTPAsnGlySerLysAspLeu 100  
 DB 603 CACAGGAGTGGAGAGCCCTTCCAAAGGCCGTCTGCAGTGGATGGAGCAAGACCTG 662  
 QY 101 GlnAspValSerIleThrValLeuAsnValThrLeuAsnAspSerGlyLeuTyrThrCys 120  
 DB 663 CAGGACGTATCCATCACTGACTCAATGTCACTTTGAATGACTCTGGCCTCTACATGC 722  
 QY 121 AsnValSerArgGluPheGluPheGluAlaHisArgProPheValLysThrThrArgLeu 140  
 DB 723 AATGTGTCAGGAGTTCGAATTCGAGGCACACAGGCCCTTTTGTGAAGACCACGAGACTG 782  
 QY 141 IleProLeuArgValThrGluGluAlaGlyGluAspPheThrSerValValSerGluIle 160  
 DB 783 ATACCTTTGCGAGTCACTGAAGAGCGGAGAGACTTCACCTCCGGTGTCTCGGAATC 842  
 QY 161 MetMetTyrIleLeuLeuValPheLeuThrLeuTyrTrpLeuLeuIleGluMetIleTyrCys 180  
 DB 843 ATGATGTACATCTCTCTGCTTCTCTCACCTGTGGCTGTTTATTAGATGATCTATTGC 902  
 QY 181 TyrArgLysValSerLysAlaGluGluAlaGlnGlnAlaGlnGlnAlaSerAspTyrLeuAla 200  
 DB 903 TACAGAAAGGTCTCTAAGGCCGAGAGGACAGCAGGAAATGCGTCTGACTACTCTTGTCT 962

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QY 201 IleProSerGluAsnLysGluAsnSerAlaValProValGluGlu 215
DB 963 ATCCCTTCAGAGAACAGAGAACTCTGTGGTACTGTGGAGGAA 1007

RESULT 8
AAC90602
ID AAC90602 standard; DNA; 2632 BP.
XX AC AAC90602;
XX 13-MAR-2001 (first entry)
DT
DE Rat sodium channel beta3 protein Alrxa94h5 related sequence.
XX
XX Rat; sodium channel beta3 protein; Alrxa94h5; pain; sleep disorder;
KW neurodegenerative disorder; mood disorder; muscle contraction; ds.
XX
XX Rattus sp.
XX WO200069912-A1.
PN
XX PD 23-NOV-2000.
XX PF 12-MAY-2000; 2000WO-US013144.
XX PR 14-MAY-1999; 99US-0134198P.
XX PA (MILL-) MILLENNIUM PHARM INC.
XX PI Curtis RAJ;
XX
XX WPI; 2001-122743/13.
DR
XX
XX New rat sodium channel beta-3 subunit gene isolated from a rat dorsal
PT root ganglion cDNA library for use in chromosome mapping, forensic
PT medicine, monitoring clinical trials and therapeutics.
XX
XX Claim 1; Page 41-42; 145pp; English.
XX
XX The present invention provides the protein and coding sequences of the
CC rat sodium channel beta3 protein, designated Alrxa94h5. This protein is
CC involved in the generation of pain and other sensory or perceptive nerve
CC impulses, in the establishment and endurance of mood, neurodegenerative
CC and sleep disorders, and in the control of muscle contraction, including
CC movements such as the heartbeat, digestion and vascular tone. The
CC sequences can be used in predictive medicine, screening and diagnostic
CC assays, and in pharmacogenomics
XX
XX Sequence 2632 BP; 693 A; 636 C; 611 G; 692 T; 0 U; 0 Other;
SQ

Alignment Scores:
Pred. No.: 1,43e-121 Length: 2632
Score: 1105.00 Matches: 211
Percent Similarity: 98.14% Conservative: 0
Best Local Similarity: 98.14% Mismatches: 4
Query Match: 98.31% Indels: 0
DB: 5 Gaps: 0

US-09-977-579A-2 (1-215) x AAC90602 (1-2632)
QY 1 MetProAlaPheAsnArgLeuPheProLeuAlaSerLeuValLeuIleTyrTrpValSer 20
DB 78 ATGCCCTTCAGAGAACAGAGAACTCTGTGGTACTGTGGTACAG 137
QY 21 ValCysPheProValCysValGluValProSerGluThrGluAlaValGlnGlyAsnPro 40
DB 138 GTCTGCTTCCTGTGTGTGGAGTGCCCTCGAGACAGAGCGGTGCAGGCGCAATCCC 197
QY 41 MetLysLeuArgCysIleSerCysMetLysArgGluGluValGluAlaThrValVal 60
DB 198 ATGAAGCTGAGGTGCATCTCCTCATGAAGAGGAGGAGGTGGAGGCGCACCACTGTGGTG 257
QY 61 GluTrpPheTyrArgProGluGlyGlyLysAspPheLeuIleTyrGluTyrArgAsnGly 80

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DB 258 GAGTGGTTCACAGGCTCTAGGCGCGTAAAGATTTCTTATATAGATTCGGAATGGC 317
QY 81 HisGlnGluValGluSerProPheGlnGlyArgLeuGlnTrpAsnGlySerLysAspLeu 100
DB 318 CACCAGGAAGTGGAGAGCCCTTCCAGGCCGCTCTGCAGTGGAAATGGAGGCAAGACCTG 377
QY 101 GlnAspValSerIleThrValLeuAsnValThrLeuAsnAspSerGlyLeuTyrThrCys 120
DB 378 CAGGACGTATCCATCATCTGTAATCAATGTCACTTTGAATGACTCTGGCCTCTACACATGC 437
QY 121 AsnValSerArgGluPheGluPheGluAlaHisArgProPheValLysThrThrArgLeu 140
DB 438 AATGTGTCAGCGAGTTCGAATTCGAGGCACACAGGCCCTTTTGTGAAGACACGAGACTG 497
QY 141 IleProLeuArgValThrGluGluAlaGlyGluAspPheThrSerValValSerGluIle 160
DB 498 ATACCTTTGGCGAGTCACCTGAAGAGCGCGGAGAACATTCACCTCCGTGGTCTCGACTACCTTGGT 557
QY 161 MetMetTyrIleLeuLeuValPheLeuThrLeuTrpLeuLeuIleGluMetIleTyrCys 180
DB 558 ATGATGTACATCCTCCTGCTCTCTCCTCAGCTTGTGGCTGTTTATTGAGATGATCTATTGC 617
QY 181 TyrArgLysValSerLysAlaGluGluAlaGlnGluAsnAlaSerAspTyrIleuAla 200
DB 618 TACAGAAAGGTCTCTAAGGCCGAAGAGGACGACAGGAAATGCGTCTGACTACCTTGGT 677
QY 201 IleProSerGluAsnLysGluAsnSerAlaValProValGluGlu 215
DB 678 ATCCCTTCAGAGAACAGAGAACTCTGTGGTACTGTGGAGGAA 722

RESULT 9
AAC90600
ID AAC90600 standard; cDNA; 3108 BP.
XX AC AAC90600;
XX 13-MAR-2001 (first entry)
DT
DE Rat sodium channel beta3 protein Alrxa94h5 coding sequence.
XX
XX Rat; sodium channel beta3 protein; Alrxa94h5; pain; sleep disorder;
KW neurodegenerative disorder; mood disorder; muscle contraction; ss.
XX
XX Rattus sp.
XX WO200069912-A1.
PN
XX PD 23-NOV-2000.
XX PF 12-MAY-2000; 2000WO-US013144.
XX PR 14-MAY-1999; 99US-0134198P.
XX PA (MILL-) MILLENNIUM PHARM INC.
XX PI Curtis RAJ;
XX
XX WPI; 2001-122743/13.
DR
XX
XX New rat sodium channel beta-3 subunit gene isolated from a rat dorsal
PT root ganglion cDNA library for use in chromosome mapping, forensic
PT medicine, monitoring clinical trials and therapeutics.
XX
XX Claim 1; Fig 1; 145pp; English.
XX
XX The present invention provides the protein and coding sequences of the
CC rat sodium channel beta3 protein, designated Alrxa94h5. This protein is
CC involved in the generation of pain and other sensory or perceptive nerve
CC impulses, in the establishment and endurance of mood, neurodegenerative
CC and sleep disorders, and in the control of muscle contraction, including
CC movements such as the heartbeat, digestion and vascular tone. The
CC sequences can be used in predictive medicine, screening and diagnostic
CC assays, and in pharmacogenomics
XX
XX movements such as the heartbeat, digestion and vascular tone. The

```

CC sequences can be used in predictive medicine, screening and diagnostic  
 CC assays, and in pharmacogenomics  
 XX  
 SQ Sequence 3108 BP; 830 A; 748 C; 727 G; 803 T; 0 U; 0 Other;

Alignment Scores:  
 Pred. No.: 1.82e-121 Length: 3108  
 Score: 1105.00 Matches: 211  
 Percent Similarity: 98.14% Conservatives: 0  
 Best Local Similarity: 98.14% Mismatches: 4  
 Query Match: 98.31% Indels: 0  
 DB: 5 Gaps: 0

US-09-977-579A-2 (1-215) x AAC90600 (1-3108)

Qy 1 MetProAlaPheAsnArgLeuPheProLeuAlaSerLeuValLeuIleTyrTrpValSer 20  
 Db ATGCTGCTTCAACAGATTGCTTCCCTAGCTTCTCTAGTGTCTCATCTACTGGGTGAGA 137  
 Qy 21 ValCysPheProValCysValGluValProSerGluThrGluAlaValGlnGlyAsnPro 40  
 Db GTCTGCTTCCCTGTGTGTGGAAGTGCCTTCGAGACAGAGCGGTGCGAGGCAATCCC 197  
 Qy 41 MetLysLeuArgCysIleSerCysMetLysArgGluGluValAlaThrThrValVal 60  
 Db ATGAAGCTGAGTGCATCTCTGATGAGAGGAGGAGGTGGAGGCCACCATGTGGTG 257  
 Qy 61 GluTrpPheTyrArgProGluGlyGlyLysAspPheLeuIleTyrGluTyrArgAsnGly 80  
 Db GAGTGGTTCACAGGCTCAGGCGGTAAGATTTCTTATATATGATATCGGAATGGC 317  
 Qy 81 HisGlnGluValGluSerProPheGlnGlyArgLeuGlnTrpAsnGlySerLysAspLeu 100  
 Db CACAGAGAGTGGAGAGCCCTTCAAGGCGGTCTGCAGTGAATGGAGCAAGACCTG 377  
 Qy 101 GlnAspValSerIleThrValLeuAsnValThrLeuAsnAspSerGlyLeuTyrThrCys 120  
 Db CAGAGCTATCATCATCTACTACTCAATGTCATTTGATGACTCTGGCTCTACATGC 437  
 Qy 121 AsnValSerArgGluPheGluPheGluAlaHisArgProPheValLysThrThrArgLeu 140  
 Db AATGTGTCAGGAGTTCGAATTCAGGACACACAGGCGCTTTGTGAAGACCAACGACTG 497  
 Qy 141 IleProLeuArgValThrGluGluAlaGlyGluAspPheThrSerValValSerGluIle 160  
 Db ATACCTTTGCGAGTCACTGAAGAGCGGGAAGACTTCACCTCCGTGGTCTCGGAATC 557  
 Qy 161 MetMetTyrIleLeuLeuValPheLeuThrLeuTrpLeuLeuIleGluMetIleTyrCys 180  
 Db ATGATGTACATCTCTCTGCTTCTTCTCACCTTGTGGCTGTTTATTTGAGATGATCTATGC 617  
 Qy 181 TyrArgLysValSerLysAlaGluGluAlaGlnGluAsnAlaSerAspTyrLeuAla 200  
 Db TACAGAAAGGTCTCTAAGCGCCGAGAGGACAGCAGAGAAATGCGTCTGACTACTTGGCT 677  
 Qy 201 IleProSerGluAsnLysGluAsnSerAlaValProValGluGlu 215  
 Db ATCCCTTCAGAGAACAGGAGAACTCTGTGGTACCTGTGGAGGAA 722

RESULT 10  
 AAK52345  
 ID AAK52345 standard; cDNA; 1045 BP.  
 XX  
 AC AAK52345;  
 XX

DT 06-NOV-2001 (first entry)

DE Human polynucleotide SEQ ID NO 890.

XX Human; cytokine; cell proliferation; cell differentiation; gene therapy;  
 KW vaccine; peptide therapy; stem cell growth factor; haematopoiesis;  
 KW tissue growth factor; immunomodulatory; cancer; leukaemia;  
 KW nervous system disorder; arthritis; inflammation; ss.

XX Homo sapiens.  
 OS  
 XX WO200157190-A2.  
 PN  
 XX 09-AUG-2001.  
 PD  
 XX 05-FEB-2001; 2001WO-US004098.  
 PF  
 XX 03-FEB-2000; 2000US-00496914.  
 PR 27-APR-2000; 2000US-00560875.  
 PR 20-JUN-2000; 2000US-00598075.  
 PR 19-JUL-2000; 2000US-00620325.  
 PR 01-SEP-2000; 2000US-00654936.  
 PR 15-SEP-2000; 2000US-00663561.  
 PR 20-OCT-2000; 2000US-00693325.  
 PR 30-NOV-2000; 2000US-00728422.  
 XX (HYSE-) HYSEQ INC.  
 PA  
 XX Tang YT, Liu C, Drmanac RT, Asundi V, Zhou P, Xu C, Cao Y;  
 PI Ma Y, Zhao QA, Wang D, Wang J, Zhang J, Ren F, Chen R, Wang ZW;  
 PI Xue AJ, Yang Y, Wejhrman T, Goodrich R;  
 XX WPI; 2001-476283/51.  
 DR P-PSDB; AAM79212.  
 XX  
 XX Nucleic acids encoding polypeptides with cytokine-like activities, useful  
 PT in diagnosis and gene therapy.  
 PT  
 XX Claim 1; Page 2934-2935; 6221pp; English.  
 PS  
 XX The invention relates to polynucleotides (AAK51456-AAK53435) and the  
 CC encoded polypeptides (AAM78323-AAM80302) that exhibit activity relating to  
 CC cytokine, cell proliferation or cell differentiation which may induce  
 CC production of other cytokines in other cell populations. The  
 CC polynucleotides and polypeptides are useful in gene therapy, vaccines or  
 CC peptide therapy. The polypeptides have various cytokine-like activities,  
 CC e.g. stem cell growth factor activity, haematopoiesis regulating  
 CC activity, tissue growth factor activity, immunomodulatory activity and  
 CC activin/inhibin activity and may be useful in the diagnosis and/or  
 CC treatment of cancer, leukaemia, nervous system disorders, arthritis and  
 CC inflammation. Note: Records for SEQ ID NO 2110 (AAK52581), 2111  
 CC (AAK52582) and 3666 (AAM80020) are omitted as the relevant pages from the  
 CC sequence listing were missing at the time of publication  
 XX  
 SQ Sequence 1045 BP; 222 A; 289 C; 314 G; 220 T; 0 U; 0 Other;

Alignment Scores:  
 Pred. No.: 1.96e-112 Length: 1045  
 Score: 1024.00 Matches: 195  
 Percent Similarity: 100.00% Conservatives: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 91.10% Indels: 0  
 DB: 4 Gaps: 0

US-09-977-579A-2 (1-215) x AAK52345 (1-1045)

Qy 1 MetProAlaPheAsnArgLeuPheProLeuAlaSerLeuValLeuIleTyrTrpValSer 20  
 Db 302 ATGCTGCTTCAATAGATTGTTTCCCTGGCTTCTCTCGTGTATCTACTGGGTGAGT 361  
 Qy 21 ValCysPheProValCysValGluValProSerGluThrGluAlaValGlnGlyAsnPro 40  
 Db 362 GTCTGCTTCCCTGTGTGTGTGGAAGTGCCTTCGAGACGAGGCGGTGCGAGGCAACCCC 421  
 Qy 41 MetLysLeuArgCysIleSerCysMetLysArgGluGluValGluAlaThrThrValVal 60  
 Db 422 ATGAAGCTGCGCTGCATCTCTGATGAAGAGAGAGAGGTGGAGGCCACCATGGTGTG 481  
 Qy 61 GluTrpPheTyrArgProGluGlyGlyLysAspPheLeuIleTyrGluTyrArgAsnGly 80  
 Db 482 GAATGGTTCACAGGCCCGAGGCGGTAAAGATTTCCTTATTACGAGTATCGGAATGGC 541

QY 81 HisGlnGluValGluSerProPheGlnGlyArgLeuGlnTrpAenGlySerLysAspLeu 100  
DB 542 CACCAGGAGGTGGAGAGCCCTTTTCAGGGGGCCCTGCAGTGGAAATGGCAGCAAGACCTG 601  
QY 101 GlnAspValSerIleThrValLeuAsnValThrLeuAsnAspSerGlyLeuTyrThrCys 120  
DB 602 CAGGACGTGTCCATCCTGCTCAACCTCACTCTGAACGACTCTGGCTCTACACCTGC 661  
QY 121 AsnValSerArgGluPheGluAlaHisArgProPheValLysThrThrArgLeu 140  
DB 662 AATGTGTCGGGAGTTTCAGTTTCAGGGCGCATCGGCCCTTTGTGAACACGACGCGGCTG 721  
QY 141 IleProLeuArgValThrGluGluAlaGlyGluAspPheThrSerValValSerGluIle 160  
DB 722 ATCCCTTAAAGAGTCACCGAGAGGCTGGAGAGGACTTCACCTCTGTGGTCTCAGAAATC 781  
QY 161 MetMetTyrIleLeuLeuValPheLeuThrLeuTrpLeuLeuIleGluMetIleTyrCys 180  
DB 782 ATGATGTACATCTTCTGCTTCTCTCACTTGTGGCTGCTCATCGAGATGATATATTC 841  
QY 181 TyrArgLysValSerLysAlaGluGluAlaGlnGluAsnAla 195  
DB 842 TACAGAAAGGTCTCAAAAGCCGAGAGGAGGAGCCCAAGAAACGCG 886

## RESULT 11

AAH98320  
ID AAH98320 standard; cdna; 978 BP.

XX AC AAH98320;

XX DT 12-OCT-2001 (first entry)

XX DE Human EST-derived coding sequence SEQ ID NO: 177.

XX KW Human; sheep; pig; cow; fruit fly; yeast; hamster; macaque; horse;  
KW tomato; monkey; dog; sea urchin; expressed sequence tag; EST;  
KW diagnostics; forensic test; gene mapping; genetic disorder; biodiversity;  
KW gene therapy; nutrition; ss.

XX OS Homo sapiens.

XX PN WO200154477-A2.

XX PD 02-AUG-2001.

XX PF 25-JAN-2001; 2001WO-US002687.

XX PR 25-JAN-2000; 2000US-00491404.

XX PR 17-JUL-2000; 2000US-00617746.

XX PR 03-AUG-2000; 2000US-00631451.

XX PR 15-SEP-2000; 2000US-00663870.

XX PA (HYSEQ-) HYSEQ INC.

XX PI Tang YT, Liu C, Zhou P, Qian XB, Wang Z, Chen R, Asundi V;

XX PI Cao Y, Drmanac RA, Zhang J, Werhman T;

XX PI WPI: 2001-476164/51.

XX DR P-PSDB; AAM23661.

XX PT Isolated polypeptide for treatment of diseases, diagnostics, raising

XX PT antibodies and research use.

XX PS Claim 1; Page 299-300; 1275pp; English.

XX CC The present invention provides the protein and coding sequences of novel  
CC proteins from a variety of organisms, including human, dog, cat, horse,  
CC cow, pig, hamster, monkey, macaque, yeast, bacteria, fruit fly, sea  
CC urchin and tomato. These were derived from expressed sequence tags (ESTs)  
CC from the organism of interest. They can be used in diagnostics,  
CC forensics, gene mapping, identification of mutations, to assess  
CC biodiversity and for nutritional purposes. The present sequence is a cDNA

## CC of the invention

XX SQ Sequence 978 BP; 193 A; 283 C; 293 G; 209 T; 0 U; 0 Other;

## Alignment Scores:

Pred. No.: 5.86e-110 Length: 978  
Score: 1003.00 Matches: 196  
Percent Similarity: 93.46% Conservative: 4  
Best Local Similarity: 91.59% Mismatches: 12  
Query Match: 89.23% Indels: 2  
DB: 4 Gaps: 0

US-09-977-579A-2 (1-215) x AAH98320 (1-978)

QY 1 MetProAlaPheAsnArgLeuPheProLeuAlaSerLeuValLeuIleTyrTrpValSer 20  
DB 295 ATGCTGCTTCAATAGATTGTTTCCCTGGCTTCTCTCGTGCTTATCTACTGGGTGAGT 354  
QY 21 ValCysPheProValCysValGluValProSerGluThrGluAlaValGlnGlyAsnPro 40  
DB 355 GTCTGCTTCCCTGTGTGTGGAAAGTGCCCTCGAGACGAGGCGCTGCAGGGCAACCCC 414  
QY 41 MetLysLeuArgCysIleSerCysMetLysArgGluValGluAlaThrThrValVal 60  
DB 415 ATGAAGCTGCGCTGCATCTCTGCAATGAAGAGAGAGAGGAGGAGGAGGAGGAGGAG 474  
QY 61 GluTrpPheTyrArgProGluGlyGlyLysAspPheLeuIleTyrGluTyrArgAsnGly 80  
DB 475 GAATGGTTCTACAGGCCCGAGGCGGTAAAGATTTCCTTATTACGAGTATCGGAATGCG 534  
QY 81 HisGlnGluValGluSerProPheGlnGlyArgLeuGlnTrpAsnGlySerLysAspLeu 100  
DB 535 CACCAGGAGGTGGAGAGCCCTTTTCAGGGGGCCCTGCAGTGGAAATGGCAGCAAGACCTG 594  
QY 101 GlnAspValSerIleThrValLeuAsnValThrLeuAsnAspSerGlyLeuTyrThrCys 120  
DB 595 CAGGACGTGTCCATCCTCACTGTCTCAACGTCACTCTGAACGACTCTGGCCCTCTACACCTGC 654  
QY 121 AsnValSerArgGluPheGluAlaHisArgProPheValLysThrThrArgLeu 140  
DB 655 AATGTGTCGGGAGTTTTCAGTTTCAGGGCGCATCGGCCCTTTGTGAACACGAGCGGCTG 714  
QY 141 IleProLeuArgValThrGluGluAlaGlyGluAspPheThrSerValValSerGluIle 160  
DB 715 ATCCCTTAAAGAGTCACCGAGGAGGCTGGAGAGGACTTCACCTCTGTGTGCTCTCAGAAATC 774  
QY 161 MetMetTyrIleLeuLeuValPheLeuThrLeuTrpLeuLeuIleGluMetIleTyrCys 180  
DB 775 ATGATGTACATCTTCTGCTTCTCTCACTTGTGGCTGCTCATCGAGATGATACATTGC 834  
QY 181 TyrArgLysValSerLysAlaGluGluAlaGlnGluAsnAlaSerAspTyrIleu-A 200  
DB 835 CTACAGAACGGGTGATCAGACGAACACGAGGCCCGCCCAAGAAACCGGATGGTACCTTTG 894  
QY 200 laileProSerGluAsnLysGluAsnSerAlaValPro 212  
DB 895 CGATTCCATTTCAGAACACGAGGAATTCCTTCGGTACCT 932

## RESULT 12

ADS11487

ID ADS11487 standard; DNA; 978 BP.

XX AC ADS11487;

XX DT 16-DEC-2004 (first entry)

XX DE Human therapeutic contig DNA - SEQ ID 1724.

XX KW antinflammatory; neuroprotective; antianaemic; cytostatic; vulnery;  
KW inflammatory; haematopoiesis; immunity; neurodegenerative; stem cell;  
KW aplastic anaemia; cancer; wound healing; gene therapy; ds; gene.  
XX OS Homo sapiens.

```

XX WO2004080148-A2.
XX
XX PD
XX
XX 23-SEP-2004.
XX
XX 30-SEP-2003; 2003WO-US030720.
XX
XX 02-OCT-2002; 2002US-0416186P.
XX
XX (NUVE-) NUVELO INC.
XX
XX Tang YT, Asundi V, Ren F, Zhang J, Zhang T, Wang Z, Ma Y;
XX Wang D, Chen R, Zhao QA, Wang J, Ghosh M, Xue AJ, Weng G, Zhou P;
XX
XX WPI; 2004-688857/65.
XX
XX DR P-PSDB; ADS12085.
XX
XX
XX New polynucleotide, useful in preparing a composition for diagnosing or
XX treating inflammatory, neurodegenerative or stem cell disorders, e.g.,
XX aplastic anemia or cancer for promoting wound healing.
XX
XX Example 2; SEQ ID NO 1724; 718pp; English.
XX
XX The invention relates to a novel isolated polynucleotide and the encoded
XX polypeptide. The molecules of the invention demonstrate antiinflammatory,
XX neuroprotective, antianaemic, cytostatic and vulnerary activities and may
XX be useful in preparing a composition for diagnosing or treating
XX inflammatory, haematopoietic, immune, neurodegenerative or stem cell
XX disorders, such as aplastic anaemia or cancer, as well as for promoting
XX wound healing. The molecules may also be utilised during gene therapy
XX procedures. The current sequence is that of a human therapeutic contig
XX DNA of the invention. The current sequence is not shown explicitly within
XX the specification but can be accessed from the WIPO web-site.
XX
XX SQ Sequence 978 BP; 193 A; 283 C; 293 G; 209 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 5,86e-110 Length: 978
Score: 1003.00 Matches: 196
Percent Similarity: 93.46% Conservative: 4
Best Local Similarity: 91.59% Mismatches: 12
Query Match: 89.23% Indels: 2
DB: 13 Gaps: 0

US-09-977-579A-2 (1-215) x ADS11487 (1-978)

Qy 1 MetProAlaPheAsnArgLeuPheProLeuAlaSerLeuValLeuIleTyrTrpValSer 20
Db
295 ATGCTGCTTCAATAGATTGTTCCCTGCTTCTCTCGTCTTATCTACTGGTCACT 354
Qy 21 ValCysPheProValCysValGluValProSerGluThrGluAlaValGlnGlyAsnPro 40
Db
355 GTCTGCTTCCCTGTGTGTGTAAGTGCCTCGGAGACGGAGCGCGTGCAGGGCAACCCC 414
Qy 41 MetLysLeuArgCysIleSerCysMetLysArgGluValGluAlaThrValVal 60
Db
415 ATGAAGTCGCTGCTGCTATCTCTGATGAAGAGAGAGAGGGTGGAGCCACCACCGTGTG 474
Qy 61 GluTrpPheTyrArgProGluGlyGlyLysAspPheLeuIleTyrGluTyrArgAsnGly 80
Db
475 GAATGGTTCTACAGGCCCGGAGCGCGTAAAGATTCTTATTACGAGTATCGGAATGGC 534
Qy 81 HisGlnGluValGluSerProPheGlnGlyArgLeuGlnTrpAsnGlySerLysAspLeu 100
Db
535 CACCAGGAGGTGGAGAGCCCTTTTCAGGGGCGCTTCAGTGGAAATGGCAGCAGGACCTG 594
Qy 101 GlnAspValSerIleThrValLeuAsnValThrLeuAsnAspSerGlyLeuTyrThrCys 120
Db
595 CAGGACGGTGCATCACTGTGCTCACTGACGACTCTGAACGACTCTGGCCTCTACACCTGC 654
Qy 121 AsnValSerArgGluPheGluAlaHisArgProPheValLysThrArgLeu 140
Db
655 AATGTGTCCTCCGGAGTTTGAGTTTGAGCGCGCATCGGCCCTTTGTGTGAACGACGCGGCTG 714

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Qy 141 IleProLeuArgValThrGluGluAlaGlyGluAspPheThrSerValValSerGluIle 160
Db
715 ATCCCCCTAAGAGTCACCGAGGAGGCTGGAGAGACTTACCTCTGTGGTCTCAGAATC 774
Qy 161 MetMetTyrIleLeuLeuValPheLeuThrLeuTrpLeuLeuIleGluMetIleTyrCys 180
Db
775 ATGATGTACATCCTTCTGGTCTTCTCCCTCACCTTGTGGCTGCTCATCGAGATGATACATGC 834
Qy 181 -TyrArgLysValSerLysAlaGluGluAlaAlaGlnGlnAsnAlaSerAspTyrLeu-A 200
Db
835 CTACAGAACGCTGATCATCAGACGAAACGAGGCCCCCAACAGAAACCGGATGGCTACCTTTG 894
Qy 200 lalleProSerGluAsnLysGluAsnSerAlaValPro 212
Db
895 CGATTTCATTTGAGAACAGGGGAAATTTCTCGGTACCT 932

RESULT 13
AAS86764
ID AAS86764 standard; cDNA; 1195 BP.
XX
XX AAS86764;
XX
XX 13-FEB-2002 (first entry)
XX
XX DNA encoding novel human diagnostic protein #22568.
XX
XX Human; chromosome mapping; gene mapping; gene therapy; forensic;
XX food supplement; medical imaging; diagnostic; genetic disorder; ss.
XX
XX Homo sapiens.
XX
XX WO200175067-A2.
XX
XX 11-OCT-2001.
XX
XX 30-MAR-2001; 2001WO-US008631.
XX
XX 31-MAR-2000; 2000US-00540217.
XX
XX 23-AUG-2000; 2000US-00649167.
XX
XX (HYSE-) HYSEQ INC.
XX
XX Drmanac RT, Liu C, Tang YT;
XX
XX WPI; 2001-639362/73.
XX
XX P-PSDB; ABG22577.
XX
XX New isolated polynucleotide and encoded polypeptides, useful in
XX diagnostics, forensics, gene mapping, identification of mutations
XX responsible for genetic disorders or other traits and to assess
XX biodiversity.
XX
XX Claim 1; SEQ ID NO 22568; 103pp; English.
XX
XX The invention relates to isolated polynucleotide (I) and polypeptide (II)
XX sequences. (I) is useful as hybridisation probes, polymerase chain
XX reaction (PCR) primers, oligomers, and for chromosome and gene mapping,
XX and in recombinant production of (II). The polynucleotides are also used
XX in diagnostics as expressed sequence tags for identifying expressed
XX genes. (I) is useful in gene therapy techniques to restore normal
XX activity of (II) or to treat disease states involving (II). (II) is
XX useful for generating antibodies against it, detecting or quantitating a
XX polypeptide in tissue, as molecular weight markers and as a food
XX supplement. (II) and its binding partners are useful in medical imaging
XX of sites expressing (II). (I) and (II) are useful for treating disorders
XX involving aberrant protein expression or biological activities. The
XX polypeptide and polynucleotide sequences have applications in
XX diagnostics, forensics, gene mapping, identification of mutations
XX and to produce other types of data and products dependent on DNA and
XX amino acid sequences. AAS64197-AAS94564 represent novel human diagnostic
XX coding sequences of the invention. Note: The sequence data for this

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CC patent did not appear in the printed specification, but was obtained in  
CC electronic format directly from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 1195 BP; 253 A; 356 C; 381 G; 205 T; 0 U; 0 Other;  
Alignment Scores:  
Pred. No.: 8, 7e-101 Length: 1195  
Score: 927.50 Matches: 184  
Percent Similarity: 94.42% Conservative: 2  
Best Local Similarity: 93.40% Mismatches: 9  
Query Match: 82.52% Indels: 2  
DB: 5 Gaps: 1

US-09-977-579A-2 (1-215) x AAS86764 (1-1195)

QY 1 MetProAlaPheAsnArgLeuPheProLeuAlaSerLeuValLeuIleTyrTrpValSer 20  
DB 463 ATGCTGCTTCAATAGATTGTTTCCCTGGCTTCTCTCGTCTTATCTAGTCACT 522

QY 21 ValCysPheProValCysValGlu-ValProSerGluThrGluAla---ValGlnGlyAs 39  
DB 523 GTCTGCTTCCCTGTGTGGGGGAAAGTGCCTTAGAAAAACGGGGGGCGGCACGGGCTAA 582

QY 39 nProMetLeuArgCysIleSerCysMetLysArgGluGluValGluAlaThrThrVa 59  
DB 583 CCCCATGAAGCTGCGCTGCTCTCTGCATGAAGAGAGAGAGGTGGAGGCCACACCGGT 642

QY 59 ValGluTrpPheTyrArgProGluGlyGlyLysAspPheLeuIleTyrGluTyrArgAs 79  
DB 643 GTTGAATGTTCTACAGGCCCGAGGGCGGTAAGATTTCCTTATTACGAGTATCGGAA 702

QY 79 nGlyHisGlnGluValGluSerProPheGlnGlyArgLeuGlnTrpAsnGlySerLysAs 99  
DB 703 TGGCCACAGGAGGTGGAGAGGCCCTTTTCAGGGGGCGCTGCAGTGGAAATGGCAGCAAGGA 762

QY 99 PleuGlnAspValSerIleThrValLeuAsnValThrLeuAsnAspSerGlyLeuTyrTh 119  
DB 763 CTGTGAGGACGTGTGCATCCTGCTCAAGCTCACTCTGAACGACTCTGGCTCTACAC 822

QY 119 rCysAsnValSerArgGluPheGluAlaHisArgProPheValLysThrThrAr 139  
DB 823 CTGCAATGTGTCGGGAGTTTGAAGTTGAGGGCGCATCGCCCTTTGTGAAGACGACGCG 882

QY 139 gLeuIleProLeuArgValThrGluGluAlaGlyLeuAspPheThrSerValValSerGl 159  
DB 883 GCTGATCCCTTAAGAGTCAACGAGGAGGCTGGAGAGGACTTCACCTCTGTGCTCTCAGA 942

QY 159 uIleMetMetTyrIleLeuLeuValPheLeuThrLeuTrpLeuLeuIleGluMetIleTy 179  
DB 943 AATCATGATGTATCATCTTCTGTGCTTCTCTCACTTGTGCTGCTCATCGAGATGATATA 1002

QY 179 rCysTyrArgLysValSerLysAlaGluGluAlaAlaGlnGluAsnAla 195  
DB 1003 TTGCTACACACAGGTCTCAAAAGCCGAGAGGAGCCCAAGAAACGCG 1051

RESULT 14  
ADS10151  
ID ADS10151 standard; DNA; 953 BP.  
XX  
AC ADS10151;  
XX  
XX  
DT 16-DEC-2004 (first entry)  
XX  
DE Human therapeutic DNA - SEQ ID 388.  
XX  
KW antiinflammatory; neuroprotective; antianaemic; cytostatic; vulnerary;  
KW inflammatory; haematopoiesis; immunity; neurodegenerative; stem cell;  
KW aplastic anaemia; cancer; wound healing; gene therapy; ds; gene.  
XX  
OS Homo sapiens.  
XX  
FN WO2004080148-A2.

XX 23-SEP-2004.  
PD  
XX  
XX 30-SEP-2003; 2003WO-US030720.  
PF  
XX 02-OCT-2002; 2002US-0416186P.  
PR  
XX (NUVE-) NUVELO INC.  
PA  
XX Tang YT, Asundi V, Ren F, Zhang J, Zhang J, Wehrman T, Wang Z, Ma Y;  
PI Wang D, Chen R, Zhao QA, Wang J, Ghosh M, Xue AJ, Weng G, Zhou P;  
XX  
XX WPI; 2004-668857/65.  
DR P-PSDB; ADS10835.  
DR  
XX New polynucleotide, useful in preparing a composition for diagnosing or  
PT treating inflammatory, neurodegenerative or stem cell disorders, e.g.,  
PT aplastic anemia or cancer for promoting wound healing.  
PS  
XX Claim 1; SEQ ID NO 388; 718pp; English.  
XX  
CC The invention relates to a novel isolated polynucleotide and the encoded  
CC polypeptide. The molecules of the invention demonstrate antiinflammatory,  
CC neuroprotective, antianaemic, cytostatic and vulnerary activities and may  
CC be useful in preparing a composition for diagnosing or treating  
CC disorders, such as aplastic anaemia or cancer, as well as for promoting  
CC inflammatory, haematopoietic, immune, neurodegenerative or stem cell  
CC wound healing. The molecules may also be utilised during gene therapy  
CC procedures. The current sequence is that of a human therapeutic DNA of  
CC the invention. The current sequence is not shown explicitly within the  
CC specification but can be accessed from the WIPO web-site.  
XX  
SQ Sequence 953 BP; 180 A; 279 C; 290 G; 204 T; 0 U; 0 Other;  
Alignment Scores:  
Pred. No.: 5, 16e-96 Length: 953  
Score: 886.50 Matches: 174  
Percent Similarity: 84.91% Conservative: 6  
Best Local Similarity: 82.08% Mismatches: 19  
Query Match: 78.87% Indels: 13  
DB: 1 Gaps: 1

US-09-977-579A-2 (1-215) x ADS10151 (1-953)

QY 1 MetProAlaPheAsnArgLeuPheProLeuAlaSerLeuValLeuIleTyrTrpValSer 20  
DB 327 ATGCTGCTTCAATAGATTGTTTCCCTGGCTTCTCTCGTCTTATCTAGTCACT 386

QY 21 ValCysPheProValCysValGluValProSerGluThrGluAlaValGlnGlyAsnPro 40  
DB 387 GTCTGCTTCCCTGTGTGTGGAAGTGCCTCGAGACGAGGCGCTGCAGGGCAACCCC 446

QY 41 MetLysLeuArgCysIleSerCysMetLysArgGluGluValGluAlaThrThrValVal 60  
DB 447 ATGAAGCTGCGCTGCATCTCTTCGATGAAGAGAGAGAGGTGGAGGCCACCGGTGGTG 506

QY 61 GluTrpPheTyrArgProGluGlyGlyLysAspPheLeuIleTyrGluTyrArgAsnGly 80  
DB 507 GAATGCTTCTACAGGCCCGAGGGCGGTAAAGATTTCCTTATTACGAGTATCGAATGCG 566

QY 81 HisGlnGluValGluSerProPheGlnGlyArgLeuGlnTrpAsnGlySerLysAspLeu 100  
DB 567 CACGAGGAGTGGAGAGGCCCTTTTCAGGGGGCGCTTCAGTGGAAATGGCAGCAAGGACCTG 626

QY 101 GlnAspValSerIleThrValLeuAsnValThrLeuAsnAspSerClyLeuTyrThrCys 120  
DB 627 CAGGAGCTGTCCATCCTGTCTCAACGTCACCTCTGAACGACTCTGGCCCTCTACACCTGC 686

QY 121 AsnValSerArgGluPheGluPheGluAlaHisArgProPheValLysThrThrArgLeu 140  
DB 687 AATGTGTCCTGGGAGTTTGAAGGCGCATTCGCCCTTTGTGAAGACGACGCGGCTG 746

QY 141 IleProLeuArgValThrGluGluAlaGlyGluAspPheThrSerValValSerGluIle 160

Db747 ATCCCTCAAGAGTCAACGAGGCTGGAGGACTTACCTCTGTGGTCTAAACACTTC806

Qy161 MetMetTyrIleLeuLeuValPheLeuThrLeuTrpLeuLeuGluMetIleTyrCys180

Db807 ATGATGTACATCCTTCTGTGGTGTCTCCACCTT-----839

Qy181 TyrArgLysValSerLysAlaGluGluAlaGlnGluAsnAlaSerAspTyrLeuAla200

Db840 -----GTGAACCAAGCCAGCTGCTCCAGAGCACTAGTGGTTCACACAGT887

Qy201 IleProSerGluAsnLysGluAsnSerAlaValPro212

Db888 GCTCTGATAGTCATCTGGGCTTCCAGCCATCCCT923

RESULT 15

AAV86895

ID AAV86895 standard; cDNA; 471 BP.

XX AC AAV86895;

XX

DT 27-APR-1999 (first entry)

XX EST clone BM4.

XX

KW Expressed sequence tag; secreted protein; haematopoiesis regulator;

KW tissue growth; activin; inhibin; tumour invasion suppressor; EST; human;

KW chemotaxis; chemokinesis; haemostasis; gene therapy; thrombolysis;

KW receptor; ligand; anti-inflammatory; tumour inhibitor; ds.

XX

OS Homo sapiens.

XX

XX WO9845435-A2.

PN

XX 15-OCT-1998.

PD

XX 10-APR-1998; 98WO-US006954.

PF

XX 10-APR-1997; 97US-00835913.

PR

XX (GENY ) GENETICS INST INC.

XX

XX Jacobs K, McCoy JM, Lavallie ER, Racie LA, Merberg D, Treacy M;

PI Spaulding V, Agostino MJ;

PI

XX WPI; 1999-070076/06.

DR

XX

XX New polynucleotides encoding human secreted proteins - derived from e.g.

PT human blood, kidney, foetal lung, placenta, testes, brain, ovary,

PT pituitary, retina and colon cDNA libraries.

PT

XX Claim 1; Page 383-384; 633pp; English.

PS

XX

XX This sequence represents an expressed sequence tag (EST), and is a

CC polynucleotide of the invention. The polynucleotides of the invention are

CC all secreted EST sequences isolated from a variety of human tissue

CC sources. The EST sequences and proteins encoded by them are predicted to

CC have useful biological activities which would make them suitable for

CC treating, preventing or ameliorating medical conditions in humans and

CC animals, although no supporting data is given. Suggested activities

CC include nutritional activity, immune stimulating or suppressing activity,

CC haematopoiesis regulating activity, tissue growth activity,

CC activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic

CC and thrombolytic activity, receptor/ligand activity, anti-inflammatory

CC activity, cadherin/tumour invasion suppressor activity, tumour inhibition

CC activity. The EST sequences are also stated to be useful for gene therapy

XX

XX Sequence 471 BP; 93 A; 126 C; 143 G; 108 T; 0 U; 1 Other;

SQ

Alignment Scores:

Pred. No.: 3.92e-79 Length: 471

Score: 742.00 Matches: 143

Percent Similarity: 98.62% Conservative: 0

Best Local Similarity: 98.62% Mismatches: 2

Query Match: 66.01% Indels: 1

DB: 2 Gaps: 0

US-09-977-579A-2 (1-215) x AAV86895 (1-471)

Qy1 MetProAlaPheAsnArgLeuPheProLeuAlaSerLeuValLeuIleTyrTrpValSer20

Db29 ATGCTCCTTCAATAGATTGTTTCCCTGGCTTCTCTCGTCTTATCTACTGGGTCACT88

Qy21 ValCysPheProValCysValGluValProSerGluThrGluAlaValGlnGlyAsnPro40

Db89 GTCTGCTTCCCTGTGTGTGAAGTCCCTCGAGACGGAGCC-GTGCANGGCAACCCC147

Qy41 MetLysLeuArgCysIleSerCysMetLysArgGluGluValGluAlaThrValVal60

Db148 ATGAAGCTGCGCTGCATCTCTGCATGAAGAGAGAGGAGGTGGAGGCCACCCGGTGGT207

Qy61 GluTrpPheTyrArgProGluGlyGlyLysAspPheLeuIleTyrGluTyrArgAsnGly80

Db208 GAATGGTTCTACAGGCCCGGCGGCTAAAGATTTCCTTATTACGAGTATCGGAATGGC267

Qy81 HisGlnGluValGluSerProPheGlnGlyArgLeuGlnTrpAsnGlySerLysAspLeu100

Db268 CACCAGGAGGTGGAGAGCCCTTTTCAGGGCGCTGCAGTGAATGGCAGCAGGACCTG327

Qy101 GlnAspValSerIleThrValLeuAsnValThrLeuAsnAspSerGlyLeuTyrThrCys120

Db328 CAGACGCTGTCCATCACTGTGCTCAACGTCACGTCGTGAACGACTCTGGCCCTCTACACCTGC387

Qy121 AsnValSerArgGluPheGluPheGluAlaHisArgProPheValLysThrThrArgLeu140

Db388 AATGTGTCCCGGAGTTTGAGTTTGAGCCGCATCGGCCCTTTGTGAAGACGACCGGCTG447

Qy141 IleProLeuArgVal145

Db448 ATCCCCCTAAAGATC462

Search completed: January 5, 2006, 19:21:05

Job time : 595 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2006 Compugen Ltd.

OM protein - nucleic search, using frame\_plus\_p2n model

Run on: January 5, 2006, 17:51:34 ; Search time 3869 Seconds

(without alignment)  
2599.954 Million cell updates/sec

Title: US-09-977-579A-2  
Perfect score: 1124  
Sequence: 1 MPANRLPPLASLVIYWS.....SDYLAIPSENKENSAPVPEE 215

Scoring table: BLOSUM62

Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 41078325 seqs, 23393541228 residues

Total number of hits satisfying chosen parameters: 82156650

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame+\_p2n.model -US09977579/runat 05012006 160653 29024/app query.fasta\_1.391  
-O=/cgn2\_1/USPTO\_spool/US09977579 -MINMATCH=0.1 -LCOOPEXT=0  
-DB=EST -QFMT=fastap -SUFFIX=rst -MINMATCH=0.1 -LCOOPEXT=0  
-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45  
-DOCALIGN=200 -THR\_SCORE=pct -THR\_MAX=100 -THR\_MIN=0 -ALIGN=15 -MODE=LOCAL  
-OUTFMT=ptc -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=2000000000  
-USER=US09977579 @CGN\_1\_1 5315 @runat 05012006 160653 29024 -ICPU=3  
-NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG  
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : EST:\*

1: gb\_est1:\*  
2: gb\_est2:\*  
3: gb\_est3:\*  
4: gb\_hic:\*  
5: gb\_est4:\*  
6: gb\_est5:\*  
7: gb\_est6:\*  
8: gb\_est7:\*  
9: gb\_gsal:\*  
10: gb\_gsal2:\*  
11: gb\_gsal3:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1124	100.0	648	10 AY419145	AY419145 Homo sapi
2	1124	100.0	2555	4 CR609664	CR609664 full-length
3	1124	100.0	4052	4 HSM801563	ALI36589 Homo sapi
4	1115	99.2	1062	5 BX420015	BX420015 BX420015
5	1097	97.6	648	10 AY419147	AY419147 Mus muscu
6	1057	97.6	1359	4 AK076466	AK076466 Mus muscu
7	1097	97.6	3549	4 AK049747	AK049747 Mus muscu

8	1084	96.4	4149	4	AK049286	AK049286 Mus muscu
9	1063	94.6	636	3	BM933157	BM933157 UI-M-BH3-
10	1061	94.4	975	5	BX445002	BX445002 BX445002
11	1051	93.5	672	2	BB614118	BB614118 BB614118
12	1042.5	92.7	4105	4	EC058083	EC058083 Mus muscu
13	977	86.9	950	2	BG294174	BG294174 602391245
14	967	85.6	582	3	BP200910	BP200910 BP200910
15	937	83.4	723	6	CA749311	CA749311 UI-M-FY0-
16	927	82.5	629	8	DR003729	DR003729 TC113490
17	868.5	77.3	927	5	BQ713131	BQ713131 AGENCOURT
18	818	72.8	584	3	BP361278	BP361278 BP361278
19	809	72.0	986	5	BUI18914	BUI18914 603142291
20	792	70.5	692	7	CN219870	CN219870 WLA010808
21	788.5	70.2	825	5	BQ745919	BQ745919 UI-M-EXO-
22	774.5	68.9	846	6	CD355879	CD355879 UI-M-FY0-
23	760	67.6	700	3	BI739617	BI739617 603361873
24	747	66.5	582	3	BP311484	BP311484 BP311484
25	747	66.5	892	5	BUI68614	BUI68614 603790206
26	745	66.3	742	6	CB526211	CB526211 UI-M-FY0-
27	744	66.2	595	5	BUI368531	BUI368531 603788820
28	737	65.6	895	5	BX743834	BX743834 BX743834
29	726	64.6	823	8	CX404153	CX404153 JGI_X2T35
30	725	64.5	821	8	CX852822	CX852822 JGI_CAA09
31	718	63.9	584	10	AY419146	AY419146 Pan_trog1
32	701	62.4	845	6	CA327438	CA327438 UI-M-FY0-
33	686.5	61.1	801	8	CX850711	CX850711 JGI_CAA07
34	683	60.8	652	2	BB652801	BB652801 BB652801
35	681	60.6	798	6	CF290312	CF290312 AGENCOURT
36	667.5	59.4	1069	3	BM928131	BM928131 AGENCOURT
37	645	57.4	450	6	CB787935	CB787935 AMGNNUC.N
38	622	55.3	734	7	CK367344	CK367344 AGENCOURT
39	618	55.0	823	7	CO428886	CO428886 UI-M-HX0-
40	606	53.9	712	6	CB526257	CB526257 UI-M-FY0-
41	600.5	53.4	901	6	CF591773	CF591773 AGENCOURT
42	583	51.9	780	5	BQ770528	BQ770528 UI-M-FY0-
43	582	51.8	750	6	CD349206	CD349206 UI-M-FY0-
44	576.5	51.3	714	6	CF531573	CF531573 UI-M-FY0-
45	570	50.7	731	8	DN010052	DN010052 JGI_CAA08

ALIGNMENTS

RESULT 1	LOCUS	AY419145	Homo sapiens HCM6793 gene, VIRTUAL TRANSCRIPT, partial sequence, genomic survey sequence.	648 bp	DNA	linear	GSS 12-DEC-2003
AY419145	DEFINITION	AY419145	AY419145	AY419145.1	GI:39775105		
ACCESSION	VERSION	AY419145	AY419145	AY419145.1	GI:39775105		
KEYWORDS	SOURCE	GSS.	Homo sapiens (human)				
ORGANISM	REFERENCE	Homo sapiens	Homo sapiens				
AUTHORS	AUTHORS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.					
		1 (bases 1 to 648)					
		Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejarawal, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.					
		Inferring nonneutral evolution from human-chimp-mouse orthologous gene trios					
TITLE	JOURNAL	Science 302 (5652), 1960-1963 (2003)					
PUBMED	PUBMED	14671302					
REFERENCE	REFERENCE	2 (bases 1 to 648)					
AUTHORS	AUTHORS	Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejarawal, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.					
		Direct Submission					
		Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA					
		These sequences were made by sequencing genomic exons and ordering					

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them based on alignment.
FEATURES             Location/Qualifiers
     source           1..648
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
     gene             <1..>648
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ORIGIN
Alignment Scores:      2.55e-126      Length:      648
Pred. No.:            1124.00      Matches:      215
Score:                100.00%      Conservative: 0
Percent Similarity:   100.00%      Mismatches:  0
Best Local Similarity: 100.00%      Indels:      0
Query Match:         100.00%      Gaps:        0
DB:                  10

US-09-977-579A-2 (1-215) x AV419145 (1-648)
Qy  1 MetProAlaPheAsnArgLeuPheProLeuAlaSerLeuValLeuIleTyrTrpValSer 20
Db  1 ATGCGTCGCTTCAATAGATTGTTTCCCGTCGGCTTCTCTCGTCTTATCTACTGGGTCA 60
Qy  21 ValCysPheProValCysValGluValProSerGluThrGluAlaValGlnGlyAsnPro 40
Db  61 GTCTGCTTCCCTGTGTGGAGTGCCTTCGGAGACGGAGCGGTGCGAGGGCAACCCC 120
Qy  41 MetLysLeuArgCysIleSerCysMetLysArgGluGluValGluAlaThrValVal 60
Db  121 ATGAAGCTGCGCTGCATCTCTCGTCATGAAGAGAGAGAGGTGGAGGCCACACCGTGTG 180
Qy  61 GluTrpPheTyrArgProGluGlyGlyLysAspPheLeuIleTyrGluTyrArgAsnGly 80
Db  181 GAATGGTTCTACAGCCCGAGGGCGGTAAAGATTTCCTTATTACGAGTATCGGAATGCG 240
Qy  81 HisGlnGluValGluSerProPheGlnGlyArgLeuGlnTrpAsnGlySerLysAspLeu 100
Db  241 CACCAGAGGTGGAGAGCCCTTTTCAGGGCGCTGTCAGTGGATGGCAGAGGACCTG 300
Qy  101 GlnAspValSerIleThrValLeuAsnValThrLeuAsnAspSerGlyLeuTyrThrCys 120
Db  301 CAGGACGTGTCCATCACTGTGCTCAACGTCACTCTGAACGACTCTGCGCTCTACACCTGC 360
Qy  121 AsnValSerArgGluPheGluPheGluAlaHisArgProPheValLysThrThrArgLeu 140
Db  361 AATGTGTCGGGAGTTTGAGTTTGGAGCGCATCGGCCCTTTGTGAAGACGACGCGGCTG 420
Qy  141 IleProLeuArgValThrGluGluAlaGlyLysAspPheThrSerValValSerGluIle 160
Db  421 ATCCCTTAAAGTACCGAGGAGGCTGGAGAGGACTTCACCTCTGTGGTCTCAGAATC 480
Qy  161 MetMetTyrIleLeuLeuValPheLeuThrLeuTrpLeuIleGluMetIleTyrCys 180
Db  481 ATGATGTACATCTTCTGCTCTTCTCACTTGTGGCTGCTCATCGAGATGATATATGC 540
Qy  181 TyrArgLysValSerLysAlaGluAlaGlnGluAsnAlaSerAspTyrLeuAla 200
Db  541 TACAGAAAGGTCTCAAAAGCCGAGAGCGACGCCCAAGAAACCGCTCTGACTACCTTGGC 600
Qy  201 IleProSerGluAsnLysGluAsnSerAlaValProValGluGlu 215
Db  601 ATCCCATCTGAGAACAAAGGAGAACTCTGCGGTACCACTGGAGGAA 645

RESULT 2
CR609664
LOCUS             CR609664      2555 bp      mRNA      linear      HTC 21-JUL-2004
DEFINITION       full-length cDNA clone CS0DF023YA09 of Fetal brain of Homo sapiens
                 (human).
ACCESSION       CR609664
VERSION         CR609664.1      GI:50490471
KEYWORDS        HTC; CNSLT. cDNA.
SOURCE          Homo sapiens (human)

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ORGANISM          Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE
  1 (bases 1 to 2555)
  Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
  Full-length cDNA libraries and normalization
  Unpublished
  JOURNAL
  REMARK
  Contact : Feng Liang Email : fliang@lifetech.com URL :
  http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
  Faraday Avenue
  Genoscope.
  2 (bases 1 to 2555)
  Direct Submission
  AUTHORS
  TITLE
  JOURNAL
  COMMENT
  1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
  end enriched, double-strand cDNA was digested with Not I and cloned
  into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
  was normalized. Library was constructed by Life Technologies, a
  division of Invitrogen.
  FEATURES
    source
    1..2555
    /organism="Homo sapiens"
    /mol_type="mRNA"
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    /clone="CS0DF023YA09"
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    /plasmid="pCMVSPORT_6"
ORIGIN
Alignment Scores:      1.82e-125      Length:      2555
Pred. No.:            1124.00      Matches:      215
Score:                100.00%      Conservative: 0
Percent Similarity:   100.00%      Mismatches:  0
Best Local Similarity: 100.00%      Indels:      0
Query Match:         100.00%      Gaps:        0
DB:                  4

US-09-977-579A-2 (1-215) x CR609664 (1-2555)
Qy  1 MetProAlaPheAsnArgLeuPheProLeuAlaSerLeuValLeuIleTyrTrpValSer 20
Db  235 ATCCCTGCGCTTCAATAGATTGTTTCCCGTCGGCTTCTCTCGTCTTATCTACTGGGTCA 294
Qy  21 ValCysPheProValCysValGluValProSerGluThrGluAlaValGlnGlyAsnPro 40
Db  295 GTCTGCTTCCCTGTGTGGAGTGCCTTCGGAGACGGAGCGCTGCAGGGCAACCCC 354
Qy  41 MetLysLeuArgCysIleSerCysMetLysArgGluValGluAlaThrThrValVal 60
Db  355 ATGAAGCTGCGCTGCATCTCTCGTCATGAAGAGAGAGAGGTGGAGGCCACACCGTGTG 414
Qy  61 GluTrpPheTyrArgProGluGlyGlyLysAspPheLeuIleTyrGluTyrArgAsnGly 80
Db  415 GAATGGTTCTACAGGCCCGGAGGCGGTAAAGATTTCCTTATTACGAGTATCGGAATGCG 474
Qy  81 HisGlnGluValGluSerProPheGlnGlyArgLeuGlnTrpAsnGlySerLysAspLeu 100
Db  475 CACCAGAGGTGGAGAGCCCTTTTCAGGGCGCTGTCAGTGGAAATGGCAGCAAGGACCTG 534
Qy  101 GlnAspValSerIleThrValLeuAsnValThrLeuAsnAspSerGlyLeuTyrThrCys 120
Db  535 CAGGACGTGTCCATCACTGTGCTCAACGTCACTCTGAAACGACTCTGCGCTCTACACCTGC 594
Qy  121 AsnValSerArgGluPheGluAlaHisArgProPheValLysThrThrArgLeu 140
Db  595 AATGTGTCGGGAGTTTGAGTTTGGAGCGCATCGGCCCTTTGTGAAGACGACGCGGCTG 654
Qy  141 IleProLeuArgValThrGluGluAlaGlyLysAspPheThrSerValValSerGluIle 160
Db  655 ATCCCTTAAAGTCAACCGAGGAGGCTGGAGAGGACTTTCACCTCTGTGGTCTCAGAATC 714

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161 MetMetTyrIleLeuLeuValPheLeuThrLeuTrrPleuLeuIleGluMetIleTyrCys 180
715 ATGATGTACATCCCTTCTGCTTCTCTACCTTGTGGCTGCTCATCGAGATGATATATGCG 774
181 TyrArgLysValSerLysAlaGluGluAlaAlaGlnGluAenAlaSerAspTyrLeuAla 200
775 TACAGAAAGGTCTCAAAAGCCGAGAGAGCAGCCCAAGAAACGGCTCTGACTACCTTGCC 834
201 IleProSerGluAenLysGluAenSerAlaValProValGluGlu 215
835 ATCCATCTGAGAACAGAGAACTCTGCGGTACCAAGTGGAGGAA 879

RESULT 3
HSM801563
LOCUS
DEFINITION Homo sapiens mRNA; cDNA DKFZp761F182 (from clone DKFZp761F182).
ACCESSION AL136589
VERSION AL136589.1 GI:13276680
KEYWORDS HTC.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1 (bases 1 to 4052)
Ottewaelder,B.; Obermaier,B., Deutschenbaur,S., Schaiipp,A.,
Mewes,H.W., Weill,B., Amid,C., Osanger,A., Fobo,G., Han,M. and
Wiemann,S.
The German cDNA Consortium
Direct Submission
Submitted (22-SEP-2004) MIPS, Ingolstaedter Landstr.1, D-85764
Neuherberg, GERMANY
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
sequenced by Medigenomix (Martinsried/Germany) within the cDNA
sequencing consortium of the German Genome Project.
This clone (DKFZp761F182) is available at the RZPD Deutsches
Ressourcenzentrum fuer Genomforschung GmbH in Berlin, Germany.
Please contact RZPD for ordering:
http://www.rzpd.de/cgi-bin/products/cl.cgi?cloneID=DKFZp761F182
Further information about the clone and the sequencing project is
available at http://mips.gsf.de/projects/cdna/.

FEATURES
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/clone_lib="761 (synonym: hamy2). Vector pSport1; host
DH10B; sites NotI + SalI"
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804..1451
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gene
CDS
ORIGIN
Alignment Scores:

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Pred. No.: 3,52e-125 Length: 4052
Score: 1124.00 Matches: 215
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0
US-09-977-579A-2 (1-215) x HSM801563 (1-4052)

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Db 804 ATGCTCTGCCCTTCAATAGATGTTTCCCTTGGCTTCTCTGCTTATCTACTGGGTCACT 863
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Db 864 GTCTGCTTCCCTTGTGTGTGGAGTGCCTTCGAGAGCGGAGCGGTGCGAGGCAACCCC 923
Qy 41 MetLysLeuArgCysIleSerCysMetLysArgGluValGluAlaThrThrValVal 60
Db 924 ATGAAGCTGGCGTGCATCTCTCGATGAAGAGAGAGAGGTGGAGGCCACCACCGTGGTG 983
Qy 61 GluTrrPheTyrArgProGluGlyGlyAspPheLeuIleTyrGluTyrArgAenGly 80
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Qy 101 GlnAspValSerIleThrValLeuAenValThrLeuAenAspSerGlyLeuTyrThrCys 120
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Qy 141 IleProLeuArgValThrGluGluAlaGlyGluAspPheThrSerValValSerGluLeu 160
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Qy 161 MetMetTyrIleLeuValPheLeuThrLeuTrrPleuLeuIleGluMetIleTyrCys 180
Db 1284 ATGATGTACATCTTCTGCTTCTCTCACTACCTTGTGGTGTCTCATCGAGATGATATATG 1343
Qy 181 TyrArgLysValSerLysAlaGluGluAlaAlaGlnGluAenAlaSerAspTyrLeuAla 200
Db 1344 TACAGAAAGGTCTCAAAAGCCGAGAGAGCAGCCCAAGAAACGGCTCTGACTACCTTGCC 1403
Qy 201 IleProSerGluAenLysGluAenSerAlaValProValGluGlu 215
Db 1404 ATCCATCTGAGAACAGAGAACTCTGCGGTACCAAGTGGAGGAA 1448

RESULT 4
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LOCUS BX420015 Homo sapiens FETAL BRAIN Homo sapiens cDNA clone
DEFINITION CS0DF023YA09 5-PRIME, mRNA sequence.
ACCESSION BX420015
VERSION BX420015.2 GI:46929710
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1 (bases 1 to 1062)
Li W.B., Gruber C., Jessee J., and Polayes D.
Full-length cDNA libraries and normalization
Unpublished (2001)
JOURNAL On May 13, 2003 this sequence version replaced gi:30646738.
COMMENT Contact: Genoscope
Genoscope - Centre National de Sequencage

```

2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE  
 Email: seque@genoscope.cns.fr, Web : www.genoscope.cns.fr  
 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime  
 end enriched, double-strand cDNA was digested with Not I and cloned  
 into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library  
 was not normalized. Library was constructed by Life Technologies, a  
 division of Invitrogen.

This sequence belongs to sequence cluster 6147.1

For more information about this cluster, see

http://www.genoscope.cns.fr/cdna?s=CS0DF023AA05QPI&c=6147.1.

## FEATURES

Location/Qualifiers  
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 /note="Organ: brain; Vector: pCMVSPORT\_6; 1st strand cDNA  
 was primed with a NotI-oligo(dT) primer. Five prime end  
 enriched, double-strand cDNA was digested with Not I and  
 cloned into the Not I and EcoRV sites of the pCMVSPORT 6  
 vector. Library was not normalized."

## ORIGIN

Alignment Scores:  
 Pred. No.: 6.51e-125 Length: 1062  
 Score: 1115.00 Matches: 214  
 Percent Similarity: 99.53% Conservative: 0  
 Best Local Similarity: 99.53% Mismatches: 1  
 Query Match: 99.20% Indels: 0  
 DB: 5 Gaps: 0

US-09-977-579A-2 (1-215) x BX420015 (1-1062)

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 Db 234 ATGCTGCTTCAATAGATTGTTTCCCTGCTGCTTCTCTGCTGCTATCTAGTGGTCACT 293

Qy 21 ValCysPheProValCysValGluValProSerGluThrGluAlaValGlnGlyAsnPro 40  
 Db 294 GTCTGCTTCCCTGTGTGTGAAGTGCCTCGAGACGAGGCGCGTGACGGCAACCCC 353

Qy 41 MetLysLeuArgCysIleSerCysMetLysArgGluGluValGluAlaThrThrValVal 60  
 Db 354 ATGAAGCTGCGCTGCATCTCTGCTGATGAAGAGAGAGAGGTGGAGGCCACACCGTGTG 413

Qy 61 GluTrpPheTyrArgProGluGlyGlyLysAspPheLeuIleTyrGluTyrArgAsnGly 80  
 Db 414 GAATGGTGTCTACAGGCCGAGCGCGGTAAAGATTTCCTTATTTACGAGTATCGGAATGGC 473

Qy 81 HisGlnGluValGluSerProPheGlnGlyArgLeuGlnTrpAsnGlySerLysAspLeu 100  
 Db 474 CACCAGAGGTGGAGAGCCCTTTTCAGGGGCGCTTCGATGGATGGCAGACGACCTG 533

Qy 101 GlnAspValSerIleThrValLeuAsnValThrLeuAsnAspSerGlyLeuTyrThrCys 120  
 Db 534 CAGGACGTGTCCATCCTGCTCAACGTCTCAACGTCTCAACGTCTGCGCTCTACACCTGC 593

Qy 121 AsnValSerArgGluPheGluPheGluAlaHisArgProPheValLysThrThrArgLeu 140  
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Qy 141 IleProLeuArgValThrGluGluAlaGlyGluAspPheThrSerValValSerGluIle 160  
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Qy 161 MetMetTyrIleLeuLeuValPheLeuThrLeuTrpLeuLeuIleGluMetIleTyrCys 180  
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Qy 181 TyrArgLysValSerLysAlaGluGluAlaAlaGlnGluAsnAlaSerAspTyrLeuAla 200

Db 774 TACAGAAGGTCTCAAAAGCGGAGAGGCGCCCAAGAAACGGCTCTGACTACCTTGCC 833

Qy 201 IleProSerGluAsnLysGluAsnSerAlaValProValGluGlu 215  
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 LOCUS Mus musculus HCM6793 gene, VIRTUAL TRANSCRIPT, partial sequence,  
 genomic survey sequence.  
 ACCESSION AY419147  
 VERSION AY419147.1 GI:39775107  
 KEYWORDS GSS.  
 SOURCE Mus musculus (house mouse)  
 ORGANISM Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;  
 Sciurognathi; Muroidea; Muridae; Murinae; Mus.  
 REFERENCE 1 (bases 1 to 648)  
 AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,  
 Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,  
 Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,  
 Adams,M.D. and Cargill,M.  
 TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous  
 gene trios  
 JOURNAL Science 302 (5652), 1960-1963 (2003)  
 PUBMED 14671302  
 REFERENCE 2 (bases 1 to 648)  
 AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,  
 Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,  
 Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,  
 Adams,M.D. and Cargill,M.  
 TITLE Direct Submission  
 JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,  
 Rockville, MD 20850, USA  
 COMMENT These sequences were made by sequencing genomic exons and ordering  
 them based on alignment.  
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 source 1. .648  
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 Alignment Scores:  
 Pred. No.: 5.06e-123 Length: 648  
 Score: 1097.00 Matches: 210  
 Percent Similarity: 97.67% Conservative: 0  
 Best Local Similarity: 97.67% Mismatches: 5  
 Query Match: 97.60% Indels: 0  
 DB: 10 Gaps: 0

US-09-977-579A-2 (1-215) x AY419147 (1-648)

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 Db 61 GTCTGCTTCCCTGTGTGTGATAGTACCTCGAGACAGAACCGGTGCGAGCAATTC 120

Qy 41 MetLysLeuArgCysIleSerCysMetLysArgGluGluValGluAlaThrThrValVal 60  
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Qy 61 GluTrpPheTyrArgProGluGlyGlyLysAspPheLeuIleTyrGluTyrArgAsnGly 80  
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Db 57 ATGCTGCTTCAACAGATTGCTTCCCTAGCTTCTCTAGTGCTCATCTACTGGGTGAGA 116

Qy 21 ValCysPheProValCysValGluValProSerGluThrGluAlaValGlnGlyAspPro 40  
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Db 297 CACCAGAGGTGGAGAGCCCTTCCAAAGTGGCTCTGAGTGGAAATGGAGCAAGACCTG 356  
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Qy 141 IleProLeuArgValThrGluGluAlaGlyGluAspPheThrSerValValSerGluIle 160  
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Db 597 TACGAAAGGTCTCTAAGCGGAGAGAGGAGCTCAGGANAATGGCTCTGACTACCTTGCT 656  
Qy 201 IleProSerGluAsnLysGluAsnSerAlaValProValGluGlu 215  
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RESULT 7

AK049747 3549 bp mRNA linear HTC 03-APR-2004

LOCUS Mus musculus 12 days embryo spinal cord cDNA, RIKEN full-length  
enriched library, clone: C530046E12 product: VOLTAGE-GATED SODIUM  
CHANNEL BETA-3 SUBUNIT (SODIUM CHANNEL BETA 3 SUBUNIT) homolog  
[Rattus norvegicus], full insert sequence.

ACCESSION AK049747

VERSION AK049747.1 GI:26340475

KEYWORDS HTC; CAP trapper.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;  
Sciurognathi; Muridae; Murinae; Mus.

1 Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,  
Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M., and Hayashizaki, Y.  
Normalization and subcloning of cap-trapper-selected cDNAs to  
prepare full-length cDNA libraries for rapid discovery of new genes  
Genome Res. 10 (10), 1617-1630 (2000)

2 10349636

REFERENCE

AUTHORS Carninci, P. and Hayashizaki, Y.

TITLE High-efficiency full-length cDNA cloning

JOURNAL Meth. Enzymol. 303, 19-44 (1999)

PUBMED 10349636

AUTHORS

TITLE

JOURNAL

PUBMED

REFERENCE

AUTHORS

Sumi, N., Itoh, M., Aizawa, K., Nagao, S., Sasaki, N., Carninci, P.,  
Konno, H., Akiyama, J., Nishi, K., Kitagawa, T., Tashiro, H., Itoh, M.,  
Sumi, N., Itoh, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A.,

Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K.,  
Fujiwaka, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M.,  
Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura, S., Kawai, J.,  
Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A., and Hayashizaki, Y.  
RIKEN integrated sequence analysis (RISA) system--384-format  
sequencing pipeline with 384 multicapillary sequencer  
Genome Res. 10 (11), 1757-1771 (2000)

11076861

4

The RIKEN Genome Exploration Research Group Phase II Team and the  
FANTOM Consortium.  
Functional annotation of a full-length mouse cDNA collection  
Nature 409, 685-690 (2001)

5

The FANTOM Consortium and the RIKEN Genome Exploration Research  
Group Phase I & II Team.  
Analysis of the mouse transcriptome based on functional annotation  
of 60,770 full-length cDNAs  
Nature 420, 563-573 (2002)

6 (bases 1 to 3549)

Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P.,  
Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W.,  
Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T.,  
Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T.,  
Kato, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M.,  
Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M.,  
Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohato, N.,  
Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N.,  
Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T.,  
Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akai, S.,  
Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A.,  
Muramatsu, M., and Hayashizaki, Y.  
Direct Submission  
Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of  
Physical and Chemical Research (RIKEN), Laboratory for Genome  
Exploration Research Group, RIKEN Genomic Sciences Center (GSC),  
RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,  
Kanagawa 230-0045, Japan (E-mail: genome-res@gsc.riken.jp,  
URL: http://genome.gsc.riken.jp/, Tel: 81-45-503-9216)  
Fax: 81-45-503-9216)

COMMENT

cDNA library was prepared and sequenced in Mouse Genome  
Encyclopedia Project of Genome Exploration Research Group in Riken  
Genomic Sciences Center and Genome Science Laboratory in Riken  
Division of Experimental Animal Research in Riken contributed to  
prepare mouse tissues.  
Please visit our web site for further details.  
URL: http://genome.gsc.riken.jp/  
URL: http://fantom.gsc.riken.jp/  
Location/Qualifiers  
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ORIGIN

Alignment Scores: 5.77e-122 Length: 3549  
Pred. No.: 1097.00 Matches: 210  
Score: 1097.00  
Percent Similarity: 97.67% Conservativeness: 0  
Best Local Similarity: 97.67% Mismatches: 5  
Query Match: 97.60% Indels: 0  
DB: 4 Gaps: 0

US-09-977-579A-2 (1-215) x AK049747 (1-3549)

QY	1	MetProAlaPheAsnArgLeuPheProLeuAlaSerLeuValLeuIleTyrTrpValSer	20
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QY	21	ValCysPheProValCysValGluValProSerGluThrGluAlaValGlnGlyAsnPro	40
DB	292	GTCTGCTTCCCTGTGTGTAGAAAGTACCCTCGAGACAGAAAGCGTGCAGGGCAATTCC	351
QY	41	MetLysLeuArgCysIleSerCysMetLysArgGluGluValGluAlaThrThrValVal	60
DB	352	ATGAAGCTGAGATGCATCTCTGTCATGAAGAGGGAGGAGGTGGAGGCCACCACTGTAGTG	411
QY	61	GluTrpPheTyrArgProGluGlyGlyLysAspPheLeuIleTyrGluTyrArgAsnGly	80
DB	412	GAGTGTCTTACAGGCGCTGAGGGCGGTAAAGATTTCTTATATATAGTATCGAAATGGC	471
QY	81	HisGlnGluValGluSerProPheGlnGlyArgLeuGlnTrpAsnGlySerLysAspLeu	100
DB	472	CACCGAGAGGTGAGAGAGCCCTTCCAAAGGTGCTGTCAGTGAATGGAGGAGCAAGACCTG	531
QY	101	GlnAspValSerIleThrValLeuAsnValThrLeuAsnAspSerGlyLeuTyrThrCys	120
DB	532	CAGACGTATCCATCACTGTTCTCAATGTCACCTCTGAATGACTCTGGCCTCTACACATGT	591
QY	121	AsnValSerArgGluPheGluPheGluAlaHisArgProPheValLysThrThrArgLeu	140
DB	592	AATGTGTCCAGGGAGTTTGAGTTTCGAAGCACACCGGCCCTTTGTGAAGACCAAGACTA	651
QY	141	IleProLeuArgValThrGluGluAlaGlyGluAspPheThrSerValValSerGluIle	160
DB	652	ATACCCCTGGAGTCTACTGAAGAGGGCGGAGAGACTTCACTCCGTGTCTCGGAATC	711
QY	161	MetMetTyrIleLeuLeuValPheLeuThrLeuTrpLeuLeuIleGluMetIleTyrCys	180
DB	712	ATGATGTACATCTCTCTGCTTCTCTCACCTGTGGCTGTATTTCAGATGATCTATTGC	771
QY	181	TyrArgLysValSerLysAlaGluGluAlaAlaGlnGluAsnAlaSerAspTyrLeuAla	200
DB	772	TACAGAAGGTCTCTAAGGCCGAAGAGGACGCTCAGGAAAAATGCGTCTGACTACCTTGT	831
QY	201	IleProSerGluAsnLysGluAsnSerAlaValProValGluGlu	215
DB	832	ATCCCTTCAGAGAACAAGAGGAGACTCTGTGTACCCCGTGGAGGAA	876

RESULT 8  
AK049286  
LOCUS  
DEFINITION Mus musculus ES cells cDNA, RIKEN full-length enriched library,  
clone:C330019I03 product:VOLTAGE-GATED SODIUM CHANNEL BETA-3  
SUBUNIT (SODIUM CHANNEL BETA 3 SUBUNIT) homolog [Rattus  
norvegicus], full insert sequence.  
ACCESSION AK049286  
VERSION AK049286.1 GI:26093400  
KEYWORDS HTC; CAP trapper.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;  
Sciurognathi; Muridae; Murinae; Mus.  
1  
REFERENCE Carninci, P. and Hayashizaki, Y.  
AUTHORS  
TITLE High-efficiency full-length cDNA cloning



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Db      7  ATGCTGCCTTCAACAGATTGCTTCCCTAGCTTCTCTAGTGCTCATCTACTGGGTGAGA 66
Qy      21 ValCysPheProValCysValGluValProSerGluThrGluAlaValGlnGlyAsnPro 40
Db      67 GTCTGCTTCCCTGTGTGTAGAAATACCTTCGGAGACAGAAAGCGGTGCAGGGCAATTCC 126
Qy      41 MetLysLeuArgCysValIleSerCysMetLysArgGluGluValGluAlaThrValVal 60
Db      127 ATGAAGCTGAGATGATCTCTCTGATGAAGAGGAGGAGGTGGAGCCACCACTGTAGTG 186
Qy      61 GluTrpPheTyrArgProGluGlyGlyLysAspPheLeuIleTyrGluTyrArgAsnGly 80
Db      187 GAGTGGTTCTACAGGCTTACAGGCGGTAAAGATTTCCTTATATATAGTAGTACGAATGGC 246
Qy      81 HisGlnGluValGluSerProPheGlnGlyArgLeuGlnTrpAsnGlySerLysAspLeu 100
Db      247 CACGAGGAGGTGGAGAGCCCTTCCAGGTGCTCTGCAGTGGAAATGGGAGCAAGACCTG 306
Qy      101 GlnAspValSerIleThrValLeuAsnValThrLeuAsnAspSerGlyLeuTyrThrCys 120
Db      307 CAGGAGCTATCCATCACTGTTCTCAATGTCATCTGAATGACTCTGGCCCTTACACATGT 366
Qy      121 AsnValSerArgGluPheGluAlaHisArgProPheValLysThrArgLeu 140
Db      367 ATGTGTCAGGGAGTTGAGTTCGAGACACACCGGCCCTTTGTGAAGACCAAGACTA 426
Qy      141 IleProLeuArgValThrGluGluAlaGlyGluAspPheThrSerValValSerGluIle 160
Db      427 ATACCCCTGCGAGTCACTGAAGAGCGGAGAGACTTCACCTCGTGGTCTCGGAATC 486
Qy      161 MetMetTyrIleLeuLeuValPheLeuThrLeuTrpLeuLeuIleGluMetIleTyrCys 180
Db      487 ATGATGTATACCTCTCTGCTTCTCACTTGTGGCTGTTTATTGAGATGATCTATTGTC 546
Qy      181 TyrArgLysValSerLysAlaGluAlaGlnGluAlaGlnGluAsnAspTyrLeuAla 200
Db      547 TACGAAGGTTCTTAAGTCTGAAGAGGAGGAGTTCAGGAATGCTCTGACTACCTTGT 606
Qy      201 IleProSerGluAsnLysGluAsnSer 209
Db      607 ATCCCTTCAGAGAACACAGAGACTCT 633

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```

RESULT 10
LOCUS    BX445002
DEFINITION BX445002 Homo sapiens FETAL BRAIN Homo sapiens cDNA clone
ACCESSION BX445002
VERSION   BX445002.2 GI:47009181
KEYWORDS EST.
SOURCE    Homo sapiens (human)
ORGANISM  Homo sapiens
          Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
          Homiidae; Homo.
REFERENCE 1 (bases 1 to 975)
AUTHORS   Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
TITLE     Full-length cDNA libraries and normalization
JOURNAL   Unpublished (2001)
COMMENT   On May 15, 2003 this sequence version replaced gi:30782286.
          Contact: Genoscope
          Genoscope - Centre National de Sequencage
          2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
          Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
          1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
          end enriched, double-strand cDNA was digested with Not I and cloned
          into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library
          was not normalized. Library was constructed by Life Technologies, a
          division of Invitrogen.
          This sequence belongs to sequence cluster 6147.r
          For more information about this cluster, see
          http://www.genoscope.cns.fr/cdna?8=CSIAF0062E05QP1&c=6147.r.
          Location/Qualifiers

```

## FEATURES

RESULT 11  
BB614118  
LOCUS  
DEFINITION

BB614118 672 bp mRNA linear EST 26-OCT-2001  
BB614118 RIKEN full-length enriched, 0 day neonate head Mus

## source

1. 975  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clones="CS0DF023YA09"  
/tissue\_type="FETAL BRAIN"  
/dev\_stage="fetal"  
/clone\_lib="Homo sapiens FETAL BRAIN"  
/note="Organ: brain; Vector: pCMVSPORT 6; 1st strand cDNA  
was primed with a NotI-oligo(dT) primer. Five prime end  
enriched, double-strand cDNA was digested with Not I and  
cloned into the Not I and EcoRV sites of the pCMVSPORT 6  
vector. Library was not normalized."

## ORIGIN

Alignment Scores:  
Pred. No.: 2,26e-118 Length: 975  
Score: 1061.00 Matches: 209  
Percent Similarity: 97.67% Conservative: 1  
Best Local Similarity: 97.21% Mismatches: 5  
Query Match: 94.40% Indels: 1  
Gaps: 0

US-09-977-579A-2 (1-215) x BX445002 (1-975)

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Qy      1 MetProAlaPheAsnArgLeuPheProLeuAlaSerLeuValLeuIleTyrTrpValSer 20
Db      235 ATGCTGCTTCATAGATTGTTTCCCTGCTTCTCTCGTGTATCTACTGGGTCACT 294
Qy      21 ValCysPheProValCysValGluValProSerGluThrGluAlaValGlnGlyAsnPro 40
Db      295 GTCTGCTTCCCTGTGTGTGGAAGTGCCTCGGAGACGAGGCGCTGCAGGCAACCC 354
Qy      41 MetLysLeuArgCysIleSerCysMetLysArgGluGluValGluAlaThrThrValVal 60
Db      355 ATGAAGCTGCGCTGCATCTCTGTCATGAAGAGAGAGAGGAGGTGGAGGCCACCAACGGTGG 414
Qy      61 GluTrpPheTyrArgProGluGlyGlyLysAspPheLeuIleTyrGluTyrArgAsnGly 80
Db      415 GAATGGTTCTACAGGCCCGAGGCGGTAAAGATTTCCTTATTACGAGTATCGAATGCG 474
Qy      81 HisGlnGluValGluSerProPheGlnGlyArgLeuGlnTrpAsnGlySerLysAspLeu 100
Db      475 CACGAGGAGGTGGAGAGCCCTTTTCAGGGCGGCTTCGAGTGGAAATGGCAGCAAGACCTG 534
Qy      101 GlnAspValSerIleThrValLeuAsnValThrLeuAsnAspSerGlyLeuTyrThrCys 120
Db      535 CAGGACGTGCTCCATCACTGCTCAACGTCACTCTGAACGACTCTGGCCCTCTACACCARC 594
Qy      121 AsnValSerArgGluPheGluAlaHisArgProPheValLysThrThrArgLeu 140
Db      595 AAWAAGTCCCGGAGTTTGAGTTTGAGGGCGCATCGGCCCTTTGTGAAGACGACGCGGCTG 654
Qy      141 IleProLeuArgValThrGluGluAlaGlyGluAspPheThrSerValValSerGluIle 160
Db      655 ATCCCCCTAAGAGTCAACGAGGAGGCTGGAGAGGACTTCACCTCTGTGTGCTCTCAGAAATC 714
Qy      161 MetMetTyrIleLeuLeuValPheLeuThrLeuTrpLeuLeuIleGluMetIleTyrCys 180
Db      715 ATGATGTATACATCTCTTCTGCTCTTCTCCCTTGTGGCTGCTCATCGAGATGATATATGTC 774
Qy      181 TyrArgLysValSerLysAlaGluAlaGlnGluAsnAlaSerAspTyrLeuAla 200
Db      775 TACGAAGGTTCTAAAGCCGAGAGGAGCGAGCGCAAGAAACGCGTCTGACTACCTTGC 834
Qy      201 IleProSerGluAsnLysGluAsnSerAlaValProValGluGlu 215
Db      835 ATCCCATCTCTGAGAACAGAGGAGAC-TCTGCGGTAMCAGTGGAGGAT 878

```



```

SOURCE      Mus musculus (house mouse)
ORGANISM    Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 4105)
Strausberg, R.L., Feingold, B.A., Grouse, L.H., Derge, J.G.,
Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,
Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,
Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Heide, F.,
Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,
Scheetz, T.E., Brownstein, M.J., Uesdin, T.B., Toshiyuki, S.,
Carninci, P., Prange, C., Raha, S.S., Iqbal, N.A., Peters, G.J.,
Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J.,
McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,
Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,
Villalón, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,
Fahey, J., Helton, E., Kettman, M., Madan, A., Rodriguez, S.,
Sanchez, A., Whitting, M., Madan, A., Young, A.C., Shevchenko, Y.,
Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, B.D.,
Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,
Butterfield, Y.S., Krzywinska, M.I., Skalska, U., Smalish, D.E.,
Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.
Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
12477932
2 (bases 1 to 4105)
Strausberg, R.
Direct Submission
Submitted (08-SEP-2003) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA
NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs-remail.nih.gov
Tissue Procurement: Dr. Jim Lin, University of Iowa
cDNA Library Preparation: M. Bento Soares, University of Iowa
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Genome Sequence Centre,
BC Cancer Agency, Vancouver, BC, Canada
info@bcgsc.bc.ca
Steven Jones, Jennifer Asano, Ian Bosdet, Yaron Butterfield,
Susanna Chan, Readman Chiu, Chris Fjell, Erin Garland, Ran Guin,
Leticia Hailao, Martin Krzywinski, Reta Kutsche, Oliver Lee, Soo
Sen Lee, Victor Ling, Carrie Mathewson, Candice McLeavy, Steven
Nesse, Pawan Pandoh, Anna-Liisa Prabhu, Parvaneh Saeedi, Jacqueline
Schein, Duane Smalish, Michael Smith, Lorraine Spence, Jeff Stott,
Michael Thorne, Miranada Teai, Natasja van den Bosch, Jill Vardy,
George Yang, Scott Zuyderduyn, Marco Marra.

Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Series: IRAC Plate: 126 Row: 1 Column: 19
This clone was selected for full length sequencing because it
passed the following selection criteria: matched mRNA gi: 23943798
This clone has the following problem: frame shifted.

FEATURES             Location/Qualifiers
     source            1..4105
                     /organism="Mus musculus"
                     /mol_type="mRNA"
                     /strain="C57BL/6"
                     /db_xref="taxon:10090"
                     /clone="IMAGE:6826414"
                     /tissue_type="Brain, mouse, 13.5,14.5,16.5,17.5 dpc"
                     /clone_lib="NIH BMAP_FY0"
                     /lab_host="DH10B"
                     /notes="Vector: pYX-ASC"

ORIGIN
Alignment Scores:

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Pred. No.:      3.21e-115      Length:      4105
Score:          1042.50        Matches:    208
Percent Similarity: 96.74%      Conservative: 0
Best Local Similarity: 96.74%    Mismatches: 6
Query Match:    92.75%         Indels:      3
DB:             4              Gaps:        1

US-09-977-579A-2 (1-215) x BC058083 (1-4105)

Qy      1 MetProAlaPheAanArgLeuPheProLeuAlaSerLeuValLeuLeuTyrTrpValSer 20
356 ATGCTCTCCCTTCAACAGATTGCTTCCCTAGCTTCTCTAGTGCTCATCTACTGGGA---- 411
Db

Qy      21 ValCysPheProValCysValGluValProSerGluThrGluAlaValGlnGlyAanPro 40
412 GTCTGCTTCCCTGTGTGTAGTAGTACCTCTCGGAGACAGAGCGGTGCGGGCAATCC 471
Db

Qy      41 MetLysLeuArgCysIleSerCysMetLysArgGluGluValGluAlaThrThrValVal 60
472 ATGAAGCTGAGATGCATCTCTCGCATGAAGAGGGAGGAGGTGGAGGCCACCACCTGTATGTG 531
Db

Qy      61 GluTrpPheTyrArgProGluGlyGlyLysAspPheLeuLeuTyrGluTyrArgAsnGly 80
532 GAGTGGTTCACAGGCTTACAGGCGGTAAAGATTTCCTTATATATAGTATCGAAATGGC 591
Db

Qy      81 HisGlnGluValGluSerProPheGlnGlyArgLeuGlnTrpAsnGlySerLysAspLeu 100
592 CACGAGAGGTGGAGAGGCCCTTCCNAGGTGCTCTGCAATGGATGGAGGCAA-CACCTG 650
Db

Qy      101 GlnAspValSerIleThrValLeuAanValThrLeuAanAspSerGlyLeuTyrThrCys 120
651 CAGGAGGTATCCATCCTGTTCTCAATGTCACTCTGAATGACTCTGGGCTCTACACATGT 710
Db

Qy      121 AsnValSerArgGluPheGluPheGluAlaHisArgProPheValLysThrThrArgLeu 140
711 AATGTGTCACGGAGTTTGGAGTTGAAGCACACCGGCCCTTTGTGAAGACCAAGACTA 770
Db

Qy      141 IleProLeuArgValThrGluGluAlaGlyGluAspPheThrSerValValSerGluLeu 160
771 ATACCCCTGGAGTCACTGAGAGAGCGGGAGAGACTTCACCTCGTGGTCTCGGAAATC 830
Db

Qy      161 MetMetTyrIleLeuLeuValPheLeuThrLeuTrpLeuLeuIleGluMetIleTyrCys 180
831 ATGATGTACATCTCTCTGCTTCTTCCACCTTGTGGCTGTTTATTGAGATGATCATTTGC 890
Db

Qy      181 TyrArgLysValSerLysAlaGluGluAlaGlnGluAanAlaSerAspTyrLeuAla 200
891 TACAGAAAGGTCTCTAAGCGCCGAGAGGAGCGCTCAGGAAAATGCGCTGTGACTACCTTGTCT 950
Db

Qy      201 IleProSerGluAanLysGluAanSerAlaValProValGluGlu 215
951 ATCCCTTCAGAGACACAGAGAGNACTCTGTGGTACCCGTGGAGGAA 995
Db

RESULT 13
BG294174
LOCUS      603291245F1 NIH_MGC_94 Mus musculus cDNA clone IMAGE:4503250 5',
DEFINITION mRNA sequence.
ACCESSION BG294174
VERSION    BG294174.1 GI:13054543
KEYWORDS   EST.
SOURCE     Mus musculus (house mouse)
ORGANISM   Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 950)
AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL   Unpublished (1999)
COMMENT   Contact: Robert Strausberg, Ph.D.
          Email: cgapbs-remail.nih.gov
          Tissue Procurement: The Cepko Laboratory

```



CDNA Library Preparation: Life Technologies, Inc.  
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
 DNA Sequencing by: Incyte Genomics, Inc.  
 Clone Distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>  
 Plate: LLAM10373 Row: i Column: 11  
 High quality sequence stop: 643.  
 Location/Qualifiers  
 1. .950  
 /organism="Mus musculus"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:10090"  
 /clone="IMAGE:4503250"  
 /tissue\_type="retina"  
 /lab\_host="DH10B (phage-resistant)"  
 /clone\_lib="NIH\_MGC\_94"  
 /note="Organ: eye; Vector: pCMV-SPORT6; Site 1: NotI;  
 Site 2: SalI; Cloned unidirectionally; oligo-dT primed.  
 Average insert size 3.3 kb. Library enriched for  
 full-length clones and constructed by Life Technologies.  
 Note: this is a NIH\_MGC Library."

# FEATURES source

Alignment Scores:  
 Pred. No.: 3.93e-108 Length: 950  
 Score: 977.00 Matches: 198  
 Percent Similarity: 93.95% Conservative: 4  
 Best Local Similarity: 92.09% Mismatches: 11  
 Query Match: 86.92% Indels: 4  
 DB: 2 Gaps: 2

US-09-977-579A-2 (1-215) x BG294174 (1-950)

Qy 1 MetProAlaPheAsnArgLeuPheProLeuAlaSerLeuValLeuIleTyrTrpValSer 20  
 Db 87 ATGCTGCTTCAACAGATTGTTCCCTAGCTTCTCTAGTGCTCATCTACTGCGTGCAGA 146  
 Qy 21 ValCysPheProValCysValGluValProSerGluThrGluAlaValGlnGlyAsnPro 40  
 Db 147 GTCTGCTTCCCTGTGTGTAGAAAGTACCCTCGAGAGACAGAGCCGTGCAGGGCAATTCC 206  
 Qy 41 MetLysLeuArgCysIleSerCysMetLysArgGluGluValGluAlaThrValVal 60  
 Db 207 ATGAAGCTGAGATGCATCTCTCTGATGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 266  
 Qy 61 GluTrpPheTyrArgProGluGlyGlyLysAspPheLeuIleTyrGluTyrArgAsnGly 80  
 Db 267 GAGTGGTTCTACAGCCTGAGGCGGTAAAGATTCTCTATATATAGTATCGAAATGGC 326  
 Qy 81 HisGlnGluValGluSerProPheGlnGlyArgLeuGlnTrpAsnGlySerLysAspLeu 100  
 Db 327 CACCAGAGGTGGAGAGCCCTTCCAGAGTGTCTGCGAGTGGAAATGGGAGCAAGACCTG 386  
 Qy 101 GlnAspValSerIleThrValLeuAsnValThrLeuAsnAspSerGlyLeuTyrThrCys 120  
 Db 387 CAGACGATATCCATCATTCTCAATGTCTCTGAATGACTCTGGCCCTACACATGT 446  
 Qy 121 AsnValSerArgGluPheGluAlaHisArgProPheValLysThrThrArgLeu 140  
 Db 447 AATGTGTCCAG-GAGTTTGTAGTTCGAAGCACCCGCGCTTTGTGAAGACCAAGACTA 505  
 Qy 141 IleProLeuArgValThrGluGluAlaGlyGluAspPheThrSerValSerGluIle 160  
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 Qy 161 MetMetTyrIleLeuValPheLeuThrLeuThrTrpLeuLeuIleGluMetIleTyrCys 180  
 Db 566 ATGATGTACATCTCTCTGGTCTTCTCACCTTGTGGCTGTTTATGTAGATGATCTATTGC 625  
 Qy 181 TyrArgLysValSerLysAlaGluAlaAlaGlnGluAsnAlaSerAspTyrLeuAla 200  
 Db 626 TACAGAAAGGTCTCTAAGGCCGGAAGAGGAGT-CAGGAAATAGCGTCTGACTACTTG--- 681

Qy 201 IleProSerGluAsnLysGluAsnSerAlaValProValGluGlu 215  
 Db 682 TATCCCTTAGAAGACAGGCAA---CCTGTGGTACCGGCGCATAG 723

## RESULT 14

BP200910  
 LOCUS  
 DEFINITION BP200910 Sugano cDNA library, amygdala Homo sapiens cDNA clone  
 AMR03894, mRNA sequence.

ACCESSION BP200910

VERSION BP200910.1 GI:52050356

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
 Homnidae; Homo.

REFERENCE 1 (bases 1 to 582)

AUTHORS Suzuki,Y., Yamashita,R., Shirota,M., Sakakibara,Y., Chiba,J.,  
 Mizushima-Sugano,J., Nakai,K. and Sugano,S.

TITLE Sequence comparison of human and mouse genes reveals a homologous  
 block structure in the promoter regions

JOURNAL Genome Res. 14 (9), 1711-1718 (2004)

COMMENT 15342556

Contact: Yutaka Suzuki

Department of Virology

Institute of Medical Science, University of Tokyo

4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan

Email: yusuzuki@ims.u-tokyo.ac.jp.

## FEATURES source

1. 582  
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 /db\_xref="taxon:9606"  
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 /tissue\_type="amygdala"  
 /clone\_lib="Sugano cDNA library, amygdala"

## ORIGIN

Alignment Scores:  
 Pred. No.: 1.32e-106 Length: 582  
 Score: 962.00 Matches: 182  
 Percent Similarity: 99.45% Conservative: 0  
 Best Local Similarity: 99.45% Mismatches: 1  
 Query Match: 85.59% Indels: 0  
 DB: 3 Gaps: 0

US-09-977-579A-2 (1-215) x BP200910 (1-582)

Qy 2 ProAlaPheAsnArgLeuPheProLeuAlaSerLeuValLeuIleTyrTrpValSerVal 21  
 Db 34 CCTGCTTCAATAGATTGTTCCCTGGCTTCTCTCGTGTCTATCTACTGGGTCAAGTGC 93  
 Qy 22 CysPheProValCysValGluValProSerGluThrGluAlaValGlnGlyAsnProMet 41  
 Db 94 TGCTTCCCTGTGTGTGGAGTGCCTCGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 153  
 Qy 42 LysLeuArgCysIleSerCysMetLysArgGluGluValGluAlaThrValValGlu 61  
 Db 154 AAGCTGCGCTGCATCTCTGCATGAAGAGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAG 213  
 Qy 62 TrpPheTyrArgProGluGlyGlyLysAspPheLeuIleTyrGluTyrArgAsnGlyHis 81  
 Db 214 TGGTTCTACAGGCCCGGAGGCGGTAAAGATTCTCTTATTTACGAGTATCGGAATGGCCAC 273  
 Qy 82 GlnGluValGluSerProPheGlnGlyArgLeuGlnTrpAsnGlySerLysAspLeuGln 101  
 Db 274 CAGAGGTGGAGAGCCCTTTTCAGGGGCGCTCGAGTGGAAATGGCAGCAAGGACCTGCAG 333  
 Qy 102 AspValSerIleThrValLeuAsnValThrLeuAsnAspSerGlyLeuTyrThrCysAsn 121  
 Db 334 GACGTGTCCATCACTGTGTCTCAACGTCACTCTGAACGACTCTGGCCTCTACACCTGCAAT 393



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122 ValSerArgGluPheGluPheGluAlaHisArgProPheValLysThrThrArgLeuile 141
Db GTGTCCTCCGGAGTTTGAGTTTGAGCGCATCGGCCCTTTGTAAGACACCGCGCTGATC 453
142 ProLeuArgValThrGluGluAlaGlyGluAspPheThrSerValSerGluileMet 161
Db CCCCTNAGAGTCACCGAGGAGGCTCGAGAGGACTTCACCTCTGTGGTCTCAGAAATCATG 513
162 MetTyrIleLeuLeuValPheLeuThrLeuThrPleuLeuileGluMetIleTyrCysTyr 181
Db ATGTATACATCTTCTGTGTCATCTCACCCTGTGGTGTCTCATCGAGATGATATATGCTTAC 573
182 ArgLysVal 184
Db AGAAAGGTC 582

RESULT 15
LOCUS CA749311
DEFINITION UI-M-FY0-cdd-k-17-0-UI-r1 NIH_BMAP_FY0 Mus musculus cDNA clone
IMAGE:6831594 5', mRNA sequence.
ACCESSION CA749311
VERSION CA749311.1 GI:25570984
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Murinae; Mus.

REFERENCE
1 (bases 1 to 723)
NIH-MGC http://mgc.ncl.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabbs-remail.nih.gov
Tissue Procurement: Dr. Jim Lin, University of Iowa
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
This clone was contributed by the Brain Molecular Anatomy Project
(BMAP)
Seq primer: pYX-5.
Location/Qualifiers
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/mol_type="mRNA"
/strain="C57BL/6"
/db_xref="taxon:10090"
/clone="IMAGE:6831594"
/tissue_type="whole brain"
/dev_stage="embryo 13.5,14.5,16.5,17.5dpc"
/lab_host="NIH BMAP FY0"
/note="Organ: Brain; Vector: pYX-Asc; Site:1: EcoR I;
Site 2: Not I; The library was constructed according
Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
1996. Denatured RNA was size fractionated on a 1% agarose
gel. First strand cDNA synthesis was primed with oligo-dT
primer containing a Not I site. Double strand cDNA was
size selected according to mRNA size fraction, ligated
with EcoR I adaptor, digested with NotI and then cloned
directionally into pYX-Asc vector. The library tag
sequence located between the Not I site and the polyA tail
is AGGAGACAG. This library was created for the University
of Iowa Brain Anatomy Project (BMAP): 'Gene discovery in the
Developing Mouse Nervous System', supported by National
Institute of Mental Health (NIMH), Hemin Chin, Ph.D.,
program coordinator."

```

## FEATURES

source

## Alignment Scores:

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Pred. No.: 2.03e-103 Length: 723
Score: 937.00 Matches: 180
Percent Similarity: 97.30% Conservative: 0
Best Local Similarity: 97.30% Mismatches: 4
Query Match: 83.36% Indels: 1
DB: 6 Gaps: 0

US-09-977-579A-2 (1-215) x CA749311 (1-723)

Qy 1 MetProAlaPheAenArgLeuPheProLeuAlaSerLeuValLeuileTyrTrpValSer 20
Db 170 ATGCTCTGCTTCAACAGATTGCTTCCCTAGCTTCTTAGTGCTCATCTACTGGGTGAGA 229
Qy 21 ValCysPheProValCysValGluValProSerGluThrGluAlaValGlnGlyAsnPro 40
Db 230 GTCTGCTTCCCTGTGTGTAGAGTAGTACCTCGGAGACAGAGCCGTCGAGGCAATTC 289
Qy 41 MetLysLeuArgCysIleSerCysMetLysArgGluGluValGluAlaThrThrValVal 60
Db 290 ATGAAGCTGAGATGCATCTCTGCATGAAGAGGAGGAGGTGGAGGCCACCACCTGTAGTG 349
Qy 61 GluTrpPheTyrArgProGluGlyGlyLysAspPheLeuileTyrGluTyrArgHengly 80
Db 350 GAGTGGTTCTACAGGCCTGAGGCGGTAAAGATTTCCTTATATATGAGTATCGAAATGGC 409
Qy 81 HisGlnGluValGluSerProPheGlnGlyArgLeuGlnTrpAsnGlySerLysAspLeu 100
Db 410 CACCAGGAGGTGGAGAGGCCCTTCCAGGTGCTCTGAGTGGATGGGAGCAAGACCTG 469
Qy 101 GlnAspValSerIleThrValLeuAsnValThrLeuAsnAspSerGlyLeuTyrThrCys 120
Db 470 CAGGAGGTATCCATCCTCACTCTCACTCTGAATGACTCTGGCTCTACACATGT 529
Qy 121 AsnValSerArgGluPheGluPheGluAlaHisArgProPheValLysThrThrArgLeu 140
Db 530 AATGTGTCAGGAGAGTTTGAGTTCGAAGCACACCGGCCCTTTGTGAAGACCACAGACTA 589
Qy 141 IleProLeuArgValThrGluGlu-AlaGlyGluAspPheThrSerValValSerGluil 160
Db 590 ATACCCCTGCGAGTCACCTGAAGAGCGGGAGAGACTTCACCTCGGTGGTCTCGGAAT 649
Qy 160 eMetMetTyrIleLeuLeuValPheLeuThrLeuThrPleuLeuileGluMetIleTyrCy 180
Db 650 CATGATGTACATCTCTCTGCTTCTCTCACCTTGTGGCTGTTTATTAGATGATCTATTG 709
Qy 180 eTyrArgLysVal 184
Db 710 CTACAGAAAGGTC 722

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Search completed: January 5, 2006, 18:57:59  
Job time : 3888 secs

## ORIGIN

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GenCore version 5.1.6  
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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: January 5, 2006, 17:54:56 ; Search time 778 Seconds

(without alignments)  
2285.239 Million cell updates/sec

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Perfect score: 1124

Sequence: 1 MPANRFLPLASLVLYWVS.....SDYLAIPISENKENSAPVVEE 215

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Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 9793542 seqs, 4134699005 residues

Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

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Database :

Published Applications NA Main:

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9: /cgn2\_6/ptodata/1/pubpna/US10E\_PUBCOMB.seq.\*  
10: /cgn2\_6/ptodata/1/pubpna/US11\_PUBCOMB.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1124	100.0	1261	3	US-09-977-579-4
2	1124	100.0	1261	9	US-10-482-834A-22
3	1105	98.3	645	5	US-10-029-191-21
4	1105	98.3	2220	3	US-09-977-579-3
5	1105	98.3	2632	5	US-10-029-191-22
6	1105	98.3	3108	3	US-10-029-191-1
7	927.5	82.5	1195	9	US-10-450-763-22568
8	694	61.7	3531	9	US-10-450-763-22567

598	53.2	600	10	US-11-060-756-2816	Sequence 2816, Ap
598	53.2	600	10	US-11-060-756-2817	Sequence 2817, Ap
598	53.2	600	10	US-11-060-756-7088	Sequence 7088, Ap
598	53.2	600	10	US-11-060-756-7089	Sequence 7089, Ap
477	42.1	657	5	US-10-029-191-23	Sequence 23, Appl
473	42.1	1335	8	US-10-723-860-2247	Sequence 2247, Ap
473	42.1	1414	8	US-10-477-272-1	Sequence 1, Appl
472	42.0	1414	9	US-10-482-834A-11	Sequence 11, Appl
472	42.0	1490	3	US-09-917-800A-1654	Sequence 1654, Ap
470	41.8	1275	10	US-11-060-756-3901	Sequence 3901, Ap
470	41.8	1275	10	US-11-060-756-8173	Sequence 8173, Ap
465	41.4	1414	9	US-10-482-834A-12	Sequence 12, Appl
408.5	36.3	621	9	US-10-450-763-22566	Sequence 22566, A
396.5	35.3	545	4	US-09-925-065A-774904	Sequence 774904,
260.5	23.2	974	6	US-10-401-916-13	Sequence 13, Appl
258.5	23.0	807	6	US-10-401-916-12	Sequence 12, Appl
234	20.8	407	7	US-10-276-774-718	Sequence 718, Appl
167	14.9	1029	7	US-10-205-331-111	Sequence 111, Appl
165.5	14.7	3583	8	US-10-723-860-6471	Sequence 6471, Ap
163.5	14.5	1929	3	US-09-960-706-472	Sequence 472, App
160.5	14.3	970	9	US-10-874-706-84	Sequence 84, Appl
160.5	14.3	983	5	US-10-053-107-11	Sequence 11, Appl
160.5	14.3	983	5	US-10-227-884-237	Sequence 237, App
160.5	14.3	983	5	US-10-230-163-237	Sequence 237, App
160.5	14.3	983	5	US-10-230-338-237	Sequence 237, App
160.5	14.3	983	5	US-10-218-631-237	Sequence 237, App
160.5	14.3	983	5	US-10-230-414-237	Sequence 237, App
160.5	14.3	983	5	US-10-213-145-11	Sequence 11, Appl
160.5	14.3	983	5	US-10-232-224-237	Sequence 237, App
160.5	14.3	983	5	US-10-216-159A-237	Sequence 237, App
160.5	14.3	983	5	US-10-218-849-237	Sequence 237, App
160.5	14.3	983	5	US-10-227-873-237	Sequence 237, App
160.5	14.3	983	5	US-10-227-883-237	Sequence 237, App
160.5	14.3	983	5	US-10-219-076-237	Sequence 237, App
160.5	14.3	983	5	US-10-230-434-237	Sequence 237, App
160.5	14.3	983	5	US-10-213-199-11	Sequence 11, Appl
160.5	14.3	983	5	US-10-219-003-237	Sequence 237, Appl

#### ALIGNMENTS

##### RESULT 1

US-09-977-579-4  
; Sequence 4, Application US/09977579

; Publication No. US20040248240A1

; GENERAL INFORMATION:

; APPLICANT: Cambridge University Technical Services

; TITLE OF INVENTION: A novel family of beta sub-unit proteins from a voltage gated so

; TITLE OF INVENTION: channel

; TITLE OF INVENTION: nucleic acids encoding them and therapeutic or diagnostic uses

; FILE REFERENCE: 674558-2001

; CURRENT APPLICATION NUMBER: US/09/977,579

; CURRENT FILING DATE: 2001-10-15

; PRIOR APPLICATION NUMBER: PCT/EP00/01783

; PRIOR FILING DATE: 2000-02-24

; PRIOR APPLICATION NUMBER: 60,129,473

; PRIOR FILING DATE: 2000-02-24

; NUMBER OF SEQ ID NOS: 47

; SOFTWARE: Patentin version 3.1

; SEQ ID NO 4

; LENGTH: 1261

; TYPE: DNA

; ORGANISM: Homo sapiens

; US-09-977-579-4

Alignment Scores:

Pred. No.: 3,53e-143 Length: 1261  
Score: 1124.00 Matches: 215  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 3 Gaps: 0

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US-09-977-579A-2 (1-215) x US-09-977-579-4 (1-1261)
Qy 1 MetProAlaPheAenArgLeuPheProLeuAlaSerLeuValLeuIleTyTrpValSer 20
Db 376 ATGCTGCTTCAATAGATTGTTTCCCTGGCTTCTCTCGTGTCTATCTACTGGGTCACT 435
Qy 21 ValCysPheProValCysValGluValProSerGluThrGluAlaValGlnGlyAsnPro 40
Db 436 GTCTGCTTCCCTGTGTGTGGAGTGCCTTCGGAGACGGAGCGCGTGCAGGGCAACCCC 495
Qy 41 MetLysLeuArgCysIleSerCysMetLysArgGluGlnValGluAlaThrValVal 60
Db 496 ATGAAGCTGGCTGCATCTCTGCTATGAAGAGAGAGAGGGTGGAGGCCACACCGTGGTG 555
Qy 61 GluTrpPheTyArgProGluGlyGlyAspPheLeuIleTyTrpGluTyArgAsnGly 80
Db 556 GAATGGTTCACAGCCCGAGGGCGGTAAAGATTTCCTTATTTACGAGTATCGGAATGGC 615
Qy 81 HisGlnGluValGluSerProPheGlnGlyArgGluGlnTrpAsnGlySerLysAspLeu 100
Db 616 CACCAGGAGGTGGAGAGCCCTTTTCAGGGGCGCTTCGAGTGAATGGCAGCAAGACCTG 675
Qy 101 GlnAspValSerIleThrValLeuAsnValThrLeuAsnAspSerGlyLeuTyThrCys 120
Db 676 CAGACGCTGCTCCATCTCACTCACTCTGAACGACTCTGGCCTCTACACCTGC 735
Qy 121 AsnValSerArgGluPheGluPheGluAlaHisArgProPheValLysThrArgLeu 140
Db 736 AATGTGTCCTGGAGTGTGAGTTCAGGGCGCATCGGCCCTTTGTGAAGACGACGCGGCTG 795
Qy 141 IleProLeuArgValThrGluGluAlaGlyGluAspPheThrSerValValSerGluIle 160
Db 796 ATCCCTTAAAGATCAGCAGGAGGCTGGAGAGACTTCACCTCTGTGGTCTCAGAAATC 855
Qy 161 MetMetTyrlleLeuLeuValPheLeuThrLeuIleGluMetIleTyTrpCys 180
Db 856 ATGATGTACATCTTCTGCTCTCTCACTCTGCTGCTGCTCATCGAGATGATATATGC 915
Qy 181 TyrArgLysValSerLysAlaGluGluAlaGlnGluAsnAlaSerAspTyLeuAla 200
Db 916 TACAGAAAGGTCTCAAAAGCCGAAAGAGAGCGCCCAAGAAACGGGTCTGTACTACCTTGGC 975

RESULT 2
US-10-482-834A-22
; Sequence 22, Application US/10482834A
; Publication No. US20050074764A1
; GENERAL INFORMATION:
; APPLICANT: Muller, John Charles
; APPLICANT: Harkin, Louise Anne
; APPLICANT: Dibbens, Michelle
; APPLICANT: Wallace, Robyn
; APPLICANT: Phillips, Hillary Anny
; APPLICANT: Heron, Sara Elizabeth
; APPLICANT: Berkovic, Samuel Frank
; APPLICANT: Scheffer, Ingrid Eileen
; APPLICANT: Bionomics Limited
; TITLE OF INVENTION: MUTATIONS IN ION CHANNELS
; FILE REFERENCE: 1386/17
; CURRENT APPLICATION NUMBER: US/10/482,834A
; CURRENT FILING DATE: 2004-01-02
; NUMBER OF SEQ ID NOS: 173
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 22
; LENGTH: 1261
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-482-834A-22
Alignment Scores:

Pred. No.: 3,53e-143 Length: 1261
Score: 1124.00 Matches: 215
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0

US-09-977-579A-2 (1-215) x US-10-482-834A-22 (1-1261)
Qy 1 MetProAlaPheAenArgLeuPheProLeuAlaSerLeuValLeuIleTyTrpValSer 20
Db 376 ATGCTGCTTCAATAGATTGTTTCCCTGGCTTCTCTCGTGTCTATCTACTGGGTCACT 435
Qy 21 ValCysPheProValCysValGluValProSerGluThrGluAlaValGlnGlyAsnPro 40
Db 436 GTCTGCTTCCCTGTGTGTGGAGTGCCTTCGGAGACGGAGCGCGTGCAGGGCAACCCC 495
Qy 41 MetLysLeuArgCysIleSerCysMetLysArgGluGlnValGluAlaThrValVal 60
Db 496 ATGAAGCTGGCTGCATCTCTGCTATGAAGAGAGAGAGGGTGGAGGCCACACCGTGGTG 555
Qy 61 GluTrpPheTyArgProGluGlyGlyAspPheLeuIleTyTrpGluTyArgAsnGly 80
Db 556 GAATGGTTCACAGCCCGAGGGCGGTAAAGATTTCCTTATTTACGAGTATCGGAATGGC 615
Qy 81 HisGlnGluValGluSerProPheGlnGlyArgGluGlnTrpAsnGlySerLysAspLeu 100
Db 616 CACCAGGAGGTGGAGAGCCCTTTTCAGGGGCGCTTCGAGTGAATGGCAGCAAGACCTG 675
Qy 101 GlnAspValSerIleThrValLeuAsnValThrLeuAsnAspSerGlyLeuTyThrCys 120
Db 676 CAGACGCTGCTCCATCTCACTCACTCTGAACGACTCTGGCCTCTACACCTGC 735
Qy 121 AsnValSerArgGluPheGluPheGluAlaHisArgProPheValLysThrArgLeu 140
Db 736 AATGTGTCCTGGAGTGTGAGTTCAGGGCGCATCGGCCCTTTGTGAAGACGACGCGGCTG 795
Qy 141 IleProLeuArgValThrGluGluAlaGlyGluAspPheThrSerValValSerGluIle 160
Db 796 ATCCCTTAAAGATCAGCAGGAGGCTGGAGAGACTTCACCTCTGTGGTCTCAGAAATC 855
Qy 161 MetMetTyrlleLeuLeuValPheLeuThrLeuIleGluMetIleTyTrpCys 180
Db 856 ATGATGTACATCTTCTGCTCTCTCACTCTGCTGCTGCTCATCGAGATGATATATGC 915
Qy 181 TyrArgLysValSerLysAlaGluGluAlaGlnGluAsnAlaSerAspTyLeuAla 200
Db 916 TACAGAAAGGTCTCAAAAGCCGAAAGAGAGCGCCCAAGAAACGGGTCTGTACTACCTTGGC 975

RESULT 3
US-10-029-191-21
; Sequence 21, Application US/10029191
; Publication No. US20020160453A1
; GENERAL INFORMATION:
; APPLICANT: CURTIS, RORY A.J.
; TITLE OF INVENTION: NOVEL GENE ENCODING A SODIUM CHANNEL BETA-3 SUBUNIT
; TITLE OF INVENTION: PROTEIN
; FILE REFERENCE: 210147.00XX/5U1
; CURRENT APPLICATION NUMBER: US/10/029,191
; CURRENT FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: 09/569,978
; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: US 60/134,198
; PRIOR FILING DATE: 1999-05-14
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 21
; LENGTH: 645
; TYPE: DNA
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; ORGANISM: Rattus sp.
US-10-029-191-21

Alignment Scores:
Pred. No.: 5,09e-141 Length: 645
Score: 1105.00 Matches: 211
Percent Similarity: 98.14% Conservatives: 0
Best Local Similarity: 98.14% Mismatches: 4
Query Match: 98.31% Indels: 0
DB: 5 Gaps: 0

US-09-977-579A-2 (1-215) x US-10-029-191-21 (1-645)

Qy 1 MetProAlaPheAsnArgLeuPheProLeuAlaSerLeuValLeuIleTyrTrpValSer 20
Db 1 ATGCTGCTTCAACAGATTGCTTCCCTAGCTTCTCTAGTGCTCATCTACTGGGTGAGA 60

Qy 21 ValCysPheProValCysValGluValProSerGluThrGluAlaValGlnGlyAsnPro 40
Db 61 GTCTGCTTCCCTGCTGTGTGGAGTGCCTTCGGAGACAGAGCGGTGCAGGGCAATCCC 120

Qy 41 MetLysLeuArgCysIleSerCysMetLysArgGluGluValGluAlaThrThrValVal 60
Db 121 ATGAAGCTGAGTGCATCTCTGTCATGAAGAGGAGGAGGTGGAGGCCACCACTGTGGTG 180

Qy 61 GluTrpPheTyrArgProGluGlyGlyLysAspPheLeuIleTyrGluTyrArgAsnGly 80
Db 181 GAGTGGTTCACAGCCCTGAGGGCGGTAAAGATTTCCTTATATATAGATATCGGAATGCG 240

Qy 81 HisGlnGluValGluSerProPheGlnGlyArgLeuGlnTrpAsnGlySerLysAspLeu 100
Db 241 CACNAGGAAGTGGAGAGCCCTTCCAGGCCGCTGTCAGTGGAAATGGGAGCAAGACCTG 300

Qy 101 GlnAspValSerIleThrValLeuAsnValThrLeuAsnAspSerGlyIleTyrThrCys 120
Db 301 CAGGAGGTATCCATCACTGTACTCAATGTCAATTTGAATGACTCTGGGCTCTACACATGC 360

Qy 121 AsnValSerArgGluPheGluPheGluAlaHisArgProPheValLysThrArgLeu 140
Db 361 AATGTGTCCAGGAGTTCGAAATTCAGGCGCACAGGCCCTTTTGTGAAGACCAAGAGACTG 420

Qy 141 IleProLeuArgValThrGluGluAlaGlyGluAspPheThrSerValValSerGluIle 160
Db 421 ATACCTTTTGGAGTCACTGAAGAGCGGGAGAGACTTCACCTCGTGGTCTCGGAATC 480

Qy 161 MetMetTyrIleLeuLeuValPheLeuThrLeuIleGluMetIleTyrCys 180
Db 481 ATGATGTATACATCTCTCTGCTTCTCCTCAGCTTGTGGCTGTTTATTGAGATGATCTATTGC 540

Qy 181 TyrArgLysValSerLysAlaGluGluAlaGlnGluAsnAlaSerAspTyrIleuAla 200
Db 541 TACAGAAAGGTCTCTAAGGCCCGAAGAGGCGAGCAGACAGGAAATGCGTCTGACTTGTCT 600

Qy 201 IleProSerGluAsnLysGluAsnSerAlaValProValGluGlu 215
Db 601 ATCCCTTCAGAACACAGGAGAACTCTGTGGTACCTGTGGAGGAA 645

RESULT 4
US-09-977-579-3
; Sequence 3, Application US/09977579
; Publication No. US20040248240A1
; GENERAL INFORMATION:
; APPLICANT: Cambridge University Technical Services
; TITLE OF INVENTION: A novel family of beta sub-unit proteins from a voltage gated sod
; TITLE OF INVENTION: channel
; TITLE OF INVENTION: nucleic acids encoding them and therapeutic or diagnostic uses b
; FILE REFERENCE: 674558-2001
; CURRENT APPLICATION NUMBER: US/09/977,579
; PRIOR FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: PCT/EP00/01783
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60,129,473
; PRIOR FILING DATE: 2000-02-24

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; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 2220
; TYPE: DNA
; ORGANISM: rat
US-09-977-579-3

Alignment Scores:
Pred. No.: 3,45e-140 Length: 2220
Score: 1105.00 Matches: 211
Percent Similarity: 98.14% Conservatives: 0
Best Local Similarity: 98.14% Mismatches: 4
Query Match: 98.31% Indels: 0
DB: 3 Gaps: 0

US-09-977-579A-2 (1-215) x US-09-977-579-3 (1-2220)

Qy 1 MetProAlaPheAsnArgLeuPheProLeuAlaSerLeuValLeuIleTyrTrpValSer 20
Db 363 ATGCTGCTTCAACAGATTGCTTCCCTAGCTTCTCTAGTGCTCATCTACTGGGTGAGA 422

Qy 21 ValCysPheProValCysValGluValProSerGluThrGluAlaValGlnGlyAsnPro 40
Db 423 GTCTGCTTCCCTGCTGTGTGGAGTGCCTTCGGAGACAGAGCGGTGCAGGGCAATCCC 482

Qy 41 MetLysLeuArgCysIleSerCysMetLysArgGluGluValGluAlaThrThrValVal 60
Db 483 ATGAAGCTGAGTGCATCTCTGTCATGAAGAGGAGGAGGTGGAGGCCACCACTGTGGTG 542

Qy 61 GluTrpPheTyrArgProGluGlyGlyLysAspPheLeuIleTyrGluTyrArgAsnGly 80
Db 543 GAGTGGTTCACAGCCCTGAGGGCGGTAAAGATTTCCTTATATATAGATATCGGAATGCG 602

Qy 81 HisGlnGluValGluSerProPheGlnGlyArgLeuGlnTrpAsnGlySerLysAspLeu 100
Db 603 CACNAGGAAGTGGAGAGCCCTTCCAGGCCGCTGTCAGTGGAAATGGGAGCAAGACCTG 662

Qy 101 GlnAspValSerIleThrValLeuAsnValThrLeuAsnAspSerGlyLeuTyrThrCys 120
Db 663 CAGGAGGTATCCATCACTGTACTCAATGTCACTTTGAATGACTCTGGGCTCTACACATGC 722

Qy 121 AsnValSerArgGluPheGluPheGluAlaHisArgProPheValLysThrThrArgLeu 140
Db 723 AATGTGTCCAGGAGTTCGAATTCAGGCGCACAGGCCCTTTTGTGAAGACCAAGAGACTG 782

Qy 141 IleProLeuArgValThrGluGluAlaGlyGluAspPheThrSerValValSerGluIle 160
Db 783 ATACCTTTTGGAGTCACTGAAGAGCGGAGAAAGACTTCACCTCGTGGTCTCGGAAATC 842

Qy 161 MetMetTyrIleLeuLeuValPheLeuThrLeuIleGluMetIleTyrCys 180
Db 843 ATGATGTATACATCTCTGCTTCTCCTCAGCTTGTGGCTGTTTATTGAGATGATCTATTGC 902

Qy 181 TyrArgLysValSerLysAlaGluGluAlaGlnGluAsnAlaSerAspTyrIleuAla 200
Db 903 TACAGAAAGGTCTCTAAGGCCCGAAGAGGCGAGCAGCAGGAAATGCGTCTGACTTGTCT 962

Qy 201 IleProSerGluAsnLysGluAsnSerAlaValProValGluGlu 215
Db 963 ATCCCTTCAGAACACAGGAGAACTCTGTGGTACCTGTGGAGGAA 1007

RESULT 5
US-10-029-191-22
; Sequence 22, Application US/10029191
; Publication No. US20020160453A1
; GENERAL INFORMATION:
; APPLICANT: CURTIS, ROY A.J.
; TITLE OF INVENTION: NOVEL GENE ENCODING A SODIUM CHANNEL BETA-3 SUBUNIT
; TITLE OF INVENTION: PROTEIN
; FILE REFERENCE: 210147.00XX/5U1
; CURRENT APPLICATION NUMBER: US/10/029,191
; CURRENT FILING DATE: 2001-12-20

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; PRIOR APPLICATION NUMBER: 09/569,978
; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: US 60/134,198
; PRIOR FILING DATE: 1999-05-14
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 22
; LENGTH: 2632
; TYPE: DNA
; ORGANISM: Rattus sp.
US-10-029-191-22

Alignment Scores:
Pred. No.: 4,49e-140 Length: 2632
Score: 1105.00 Matches: 211
Percent Similarity: 98.14% Conservativeness: 0
Best Local Similarity: 98.14% Mismatches: 4
Query Match: 98.31% Indels: 0
DB: 5 Gaps: 0

US-09-977-579A-2 (1-215) x US-10-029-191-22 (1-2632)

Qy 1 MetProAlaPheAsnArgLeuPheProLeuAlaSerLeuValLeuIleTyrTrpValSer 20
Db 78 ATGCTGCCTTCACAGATTGCTTCCCTAGCTTCTCTAGTGCTCATCTACTGGGTGAGA 137

Qy 21 ValCysPheProValCysValGluValProSerGluThrGluAlaValGlnGlyAsnPro 40
Db 138 GTCTGCTTCCCTGTGTGGAGTGCCTTCGGAGACAGAGCGGTGCAGGGCAATCCC 197

Qy 41 MetLysLeuArgCysIleSerCysMetLysArgGluGluValGluAlaThrValVal 60
Db 198 ATGAAGCTGAGGTGCATCTCTCGATGAAGAGGAGGAGGTGGAGGCCACCACTGTGGTG 257

Qy 61 GluTrpPheTyrArgProGluGlyGlyLysAspPheLeuIleTyrGluTyrArgAsnGly 80
Db 258 GAGTGGTTCACAGCCCTGAGGCGGTAAAGATTTCCTTATATATAGTATCGGAATGGC 317

Qy 81 HisGlnGluValGluSerProPheGlnGlyArgLeuGlnTrpAsnGlySerLysAspLeu 100
Db 318 CACAGGAAGTGGAGAGCCCTTCCAGGCCGTCTGCAGTGGAAATGGAGCAAGACCTG 377

Qy 101 GlnAspValSerIleThrValLeuAsnValThrLeuAsnAspSerGlyLeuTyrThrCys 120
Db 378 CAGGACGTATCCATCACTGTAATCAATGTCAATTTGAATGACTCTGGCCTCTACACATGC 437

Qy 121 AsnValSerArgGluPheGluAlaHisArgProPheValLysThrArgLeu 140
Db 438 AATGTGTCAGGGAGTTCGAATTCGAGGCACACAGGCCCTTTTGTGAAGACCACGAGACTG 497

Qy 141 IleProLeuArgValThrGluGluAlaGlyGluAspPheThrSerValValSerGluIle 160
Db 498 ATACCTTTGGAGTCACTGAAGAGCGGAGAGACTTCACCTCCGTGGTCTCGGAATC 557

Qy 161 MetMetTyrIleLeuLeuValPheLeuThrLeuTrpLeuLeuIleGluMetIleTyrCys 180
Db 558 ATGATGTACATCCCTCGTCTCTCTACCTTGTGGCTGTTTATTTAGATGATCTATTGC 617

Qy 181 TyrArgLysValSerLysAlaGluAlaGlnGluAsnAlaSerAspTyrLeuAla 200
Db 618 TACAGAAAGTCTCTAAGGCCGAGAGGCAGACAGGAAATGCGTCTGACTACCTTGCT 677

Qy 201 IleProSerGluAsnLysGluAsnSerAlaValProValGluGlu 215
Db 678 ATCCCTTCAGAGAACAGGAGAACTCTGTGGTACCTGTGGAGGAA 722
```

## RESULT 6

```
US-10-029-191-1
; Sequence 1, Application US/10029191
; Publication No. US20020160453A1
; GENERAL INFORMATION:
; APPLICANT: CURTIS, ROY A.J.
; TITLE OF INVENTION: NOVEL GENE ENCODING A SODIUM CHANNEL BETA-3 SUBUNIT
```

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; TITLE OF INVENTION: PROTEIN
; FILE REFERENCE: 210147.00XX/SUI
; CURRENT APPLICATION NUMBER: US/10/029,191
; CURRENT FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: 09/569,978
; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: US 60/134,198
; PRIOR FILING DATE: 1999-05-14
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 3108
; TYPE: DNA
; ORGANISM: Rattus sp.
US-10-029-191-1

Alignment Scores:
Pred. No.: 5,81e-140 Length: 3108
Score: 1105.00 Matches: 211
Percent Similarity: 98.14% Conservativeness: 0
Best Local Similarity: 98.14% Mismatches: 4
Query Match: 98.31% Indels: 0
DB: 5 Gaps: 0

US-09-977-579A-2 (1-215) x US-10-029-191-1 (1-3108)

Qy 1 MetProAlaPheAsnArgLeuPheProLeuAlaSerLeuValLeuIleTyrTrpValSer 20
Db 78 ATGCTGCCTTCACAGATTGCTTCCCTAGCTTCTCTAGTGCTCATCTACTGGGTGAGA 137

Qy 21 ValCysPheProValCysValGluValProSerGluThrGluAlaValGlnGlyAsnPro 40
Db 138 GTCTGCTTCCCTGTGTGGAGTGCCTTCGGAGACAGAGCGGTGCAGGGCAATCCC 197

Qy 41 MetLysLeuArgCysIleSerCysMetLysArgGluGluValGluAlaThrValVal 60
Db 198 ATGAAGCTGAGGTGCATCTCTCGATGAAGAGGAGGAGGTGGAGGCCACCACTGTGGTG 257

Qy 61 GluTrpPheTyrArgProGluGlyGlyLysAspPheLeuIleTyrGluTyrArgAsnGly 80
Db 258 GAGTGGTTCACAGCCCTGAGGCGGTAAAGATTTCCTTATATATAGTATCGGAATGGC 317

Qy 81 HisGlnGluValGluSerProPheGlnGlyArgLeuGlnTrpAsnGlySerLysAspLeu 100
Db 318 CACAGGAAGTGGAGAGCCCTTCCAGGCCGTCTGCAGTGGAAATGGAGCAAGACCTG 377

Qy 101 GlnAspValSerIleThrValLeuAsnValThrLeuAsnAspSerGlyLeuTyrThrCys 120
Db 378 CAGGACGTATCCATCACTGTAATCAATGTCAATTTGAATGACTCTGGCCTCTACACATGC 437

Qy 121 AsnValSerArgGluPheGluAlaHisArgProPheValLysThrArgLeu 140
Db 438 AATGTGTCAGGGAGTTCGAATTCGAGGCACACAGGCCCTTTTGTGAAGACCACGAGACTG 497

Qy 141 IleProLeuArgValThrGluGluAlaGlyGluAspPheThrSerValValSerGluIle 160
Db 498 ATACCTTTGGAGTCACTGAAGAGCGGAGAGACTTCACCTCCGTGGTCTCGGAATC 557

Qy 161 MetMetTyrIleLeuLeuValPheLeuThrLeuTrpLeuLeuIleGluMetIleTyrCys 180
Db 558 ATGATGTACATCCCTCGTCTCTCTACCTTGTGGCTGTTTATTTAGATGATCTATTGC 617

Qy 181 TyrArgLysValSerLysAlaGluAlaGlnGluAsnAlaSerAspTyrLeuAla 200
Db 618 TACAGAAAGTCTCTAAGGCCGAGAGGCAGACAGGAAATGCGTCTGACTACCTTGCT 677

Qy 201 IleProSerGluAsnLysGluAsnSerAlaValProValGluGlu 215
Db 678 ATCCCTTCAGAGAACAGGAGAACTCTGTGGTACCTGTGGAGGAA 722
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## RESULT 7

```
US-10-450-763-22568
; Sequence 22568, Application US/10450763
```

Publication No. US20050196754A1  
GENERAL INFORMATION:  
APPLICANT: Hyseq, Inc  
TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES  
FILE REFERENCE: 790CIP3/US  
CURRENT APPLICATION NUMBER: US/10/450,763  
CURRENT FILING DATE: 2003-06-11  
PRIORITY APPLICATION NUMBER: PCT/US01/08631  
PRIORITY FILING DATE: 2001-03-30  
PRIORITY APPLICATION NUMBER: 09/540,217  
PRIORITY FILING DATE: 2000-03-31  
PRIORITY APPLICATION NUMBER: 09/649,167  
PRIORITY FILING DATE: 2000-08-23  
NUMBER OF SEQ ID NOS: 60736  
SOFTWARE: Custom  
SEQ ID NO 22568  
LENGTH: 1195  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: SIMILAR  
LOCATION: (518)..(1051)  
OTHER INFORMATION: 91% homologous to Homo sapiens voltage-gated sodium channel  
OTHER INFORMATION: beta-3 subunit, accession number AJ243396, Smith-Waterman Score=826  
US-10-450-763-22568  
Alignment Scores:  
Pred. No.: 3,17e-116 Length: 1195  
Score: 927.50 Matches: 184  
Percent Similarity: 94.42% Conservative: 2  
Best Local Similarity: 93.40% Mismatches: 9  
Query Match: 82.52% Indels: 2  
DB: 9 Gaps: 1  
US-09-977-579A-2 (1-215) x US-10-450-763-22568 (1-1195)  
QY 1 MetProAlaPheAsnArgLeuPheProLeuAlaSerLeuValLeuIleTyrTrpValSer 20  
DB 463 ATGCTGCTCCCAATAGATTGTTCCCTGGCTTCTCTGCTGCTATCTACTGAGTCAGT 522  
QY 21 ValCysPheProValCysValGlu-ValProSerGluThrGluAla---ValGlnGlyAs 39  
DB 523 GTCTGCTCCCTGCTGGGGGAAAGTGCCCTTAGAAACGGGGGGCGGCAGCGGCTAA 582  
QY 39 nProMetLysLeuArgCysIleSerCysMetLysArgGluGluValGluAlaThrVa 59  
DB 583 CCCCATGAAGCTGCGCTGCATCTCTGTCATGAAGAGAGAGAGGTGGAGGCCACCACGGT 642  
QY 59 lValGluTrpPheTyrArgProGluGlyGlyLysAspPheLeuIleTyrGluTyrArgAs 79  
DB 643 GGTGGAATGGTTCTACAGCCCGAGGGCGGTAAAGATTTCCTTATTACGAGTATCGGAA 702  
QY 79 nGlyHisGlnGluValGluSerProPheGlnGlyArgLeuGlnTrpAsnGlySerLysAs 99  
DB 703 TGCCACACAGAGAGGTGGAGAGCCCTTTTCAGGGGGCGCTGAGTGGATGGCAGCAGGA 762  
QY 99 pLeuGlnAspValSerIleThrValLeuAsnValThrLeuAsnAspSerGlyLeuTyrTh 119  
DB 763 CTGCAGGAGGTTCCATCACTGTGCTCAACGCTCACTCTGAACGACTCTGGCCTCTACAC 822  
QY 119 rCysAsnValSerArgGluPheGluPheGluAlaHisArgProPheValLysThrAr 139  
DB 823 CTGCAATGTGTCGCGGAGTTTGAGTTTGAGGCGCATCGGCCCTTTGTGAAGACACCGCG 882  
QY 139 gLeuIleProLeuArgValThrGluGluAlaGlyGluAspPheThrSerValValSerG1 159  
DB 883 GCTGATCCCCCTCAGAGTCACGAGGAGGCTGGAGGAGACTTCACCTCTGTGCTCTCAGA 942  
QY 159 uIleMetMetTyrIleLeuLeuValPheLeuThrLeuTrpLeuLeuIleGluMetIleTyr 179  
DB 943 AATCATGATGATACATCTTCTGCTCTTCTCACCCTGTGCTGCTCATCGAGATGATATA 1002  
QY 179 rCysTyrArgLysValSerLysAlaGluGluAlaGlnGluAsnAla 195

Db 1003 TTGCTACAGACAGGTCTCAAAAGCCGAAGGAGCGAGCCCAAGAAACGCG 1051  
RESULT 8  
US-10-450-763-22567  
Sequence 22567, Application US/10450763  
Publication No. US20050196754A1  
GENERAL INFORMATION:  
APPLICANT: Hyseq, Inc  
TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES  
FILE REFERENCE: 790CIP3/US  
CURRENT APPLICATION NUMBER: US/10/450,763  
CURRENT FILING DATE: 2003-06-11  
PRIORITY APPLICATION NUMBER: PCT/US01/08631  
PRIORITY FILING DATE: 2001-03-30  
PRIORITY APPLICATION NUMBER: 09/540,217  
PRIORITY FILING DATE: 2000-03-31  
PRIORITY APPLICATION NUMBER: 09/649,167  
PRIORITY FILING DATE: 2000-08-23  
NUMBER OF SEQ ID NOS: 60736  
SOFTWARE: Custom  
SEQ ID NO 22567  
LENGTH: 3531  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: SIMILAR  
LOCATION: (300)..(407)  
OTHER INFORMATION: 94% homologous to Homo sapiens putative kruppel-related zinc  
OTHER INFORMATION: finger protein NY-REN-23 antigen, accession number AF155101, Smith-  
OTHER INFORMATION: Waterman Score=180.  
US-10-450-763-22567  
Alignment Scores:  
Pred. No.: 2e-83 Length: 3531  
Score: 694.00 Matches: 130  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 61.74% Indels: 0  
DB: 9 Gaps: 0  
US-09-977-579A-2 (1-215) x US-10-450-763-22567 (1-3531)  
QY 19 ValSerValCysPheProValCysValGluValProSerGluThrGluAlaValGlnGly 38  
DB 2959 GTGAGTGTCTCCCTGCTGCTGTGTGGAAGTGCCTCGAGAGCGAGCGCGTCAGGCG 3018  
QY 39 AsnProMetLysLeuArgCysIleSerCysMetLysArgGluGluValGluAlaThrThr 58  
DB 3019 AACCCCATGAAGCTGCGCTGCATCTCTGTCATGAAGAGAGAGAGGTGGAGGCCACCAG 3078  
QY 59 ValValGluTrpPheTyrArgProGluGlyGlyLysAspPheLeuIleTyrGluTyrArg 78  
DB 3079 GTGGTGGAAATGGTTCTACAGGCCCGGCGGTAAAGATTTCCTTATTACGAGTATCGG 3138  
QY 79 AsnGlyHisGlnGluValGluSerProPheGlnGlyArgLeuGlnTrpAsnGlySerLys 98  
DB 3139 AATGCCACACAGAGAGGTGGAGAGCCCTTTTCAGGGGGCGCTGAGTGGATGGCAGCAG 3198  
QY 99 AspLeuGlnAspValSerIleThrValLeuAsnValThrLeuAsnAspSerGlyLeuTyr 118  
DB 3199 GACCTGCAGGAGCGTGTCCATCACTGTCTCAACGCTCACTCTGAACGACTCTGGCCTCTAC 3258  
QY 119 ThrCysAsnValSerArgGluPheGluPheGluAlaHisArgProPheValLysThrThr 138  
DB 3259 ACCTGCAATGTGTCCCGGAGTTTGAGTTTGAGGCGCATCGGCCCTTTGTGAAGACGAG 3318  
QY 139 ArgLeuIleProLeuArgValThrGluGlu 148  
DB 3319 CGGCTGATCCCCCTTAAGAGTCAACGAGGAG 3348  
RESULT 9  
US-11-060-756-2816





Db 123 ACAGCGGGCTGATCCCTTAAGAGTACCAGGAGGGCTGGAGAGGACTTTCACCTCTGTG 182  
Qy 157 ValSerGluIleMetMetTyrIleLeuLeuValPheLeuThrLeuTrpLeuLeuIleGlu 176  
Db 183 GTCTCAGAAATCATGATGATACATCTCTGCTCTTCTTCCCTCACCTGTGGCTCTCATCGAG 242  
Qy 177 MetIleTyrCysTyrArgLysValSerLysAlaGluAlaAaGlnGluAsnAlaSer 196  
Db 243 ATGATATATTGCTACAGAAAGGTCTCAAAAGCCGAGAGGAGCCCAAGAAAACCGCTCT 302  
Qy 197 AspTyrLeuAlaIleProSerGluAsnLysGluAsnSerAlaValProValGluGlu 215  
Db 303 GACTACCTTGCCATCCATCTGAGAACCAAGAGAACTCTGCGGTACCACTGAGGAGAA 359

## RESULT 12

US-11-060-756-7089  
; Sequence 7089, Application US/11060756  
; Publication No. US20050221354A1  
; GENERAL INFORMATION:  
; APPLICANT: Wyeth  
; TITLE OF INVENTION: Mounts, William Martin  
; FILE REFERENCE: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug  
; CURRENT APPLICATION NUMBER: US/11/060,756  
; NUMBER OF SEQ ID NOS: 2005-02-18  
; SOFTWARE: Patent In version 3.2  
; SEQ ID NO 7089  
; LENGTH: 600  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-11-060-756-7089

Alignment Scores:  
Pred. No.: 1,988-71 Length: 600  
Score: 598.00 Matches: 119  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 53.20% Indels: 0  
DB: 10 Gaps: 0

US-09-977-579A-2 (1-215) x US-11-060-756-7089 (1-600)

Qy 97 SerLysAspLeuGluAspValSerIleThrValLeuAsnValThrIleuAsnAspSergly 116  
Db 3 AGCAAGGACCTGCAGAGCGTGTCTCATCTGCTCACTGCTCACTGCTCACTGCTCACTGCTG 62  
Qy 117 LeuTyrThrCysAsnValSerArgGluPheGluAlaAaGlnGluAsnValPheValLys 136  
Db 63 CTCTACACTGCAATGTGCTCCGAGAGTTTGAGTTTGAGGCGCATCGGCCCTTTGTGAAG 122  
Qy 137 ThrThrArgLeuIleProLeuArgValThrGluGluAlaGlyGluAspPheThrSerVal 156  
Db 123 ACAGCGGGCTGATCCCTTAAGAGTACCAGGAGGCTGGAGAGGACTTCACTCTGTG 182  
Qy 157 ValSerGluIleMetMetTyrIleLeuLeuValPheLeuThrLeuTrpLeuLeuIleGlu 176  
Db 183 GTCTCAGAAATCATGATGATACATCTCTGCTCTTCTCCTCACCTGTGCTGCTCATCGAG 242  
Qy 177 MetIleTyrCysTyrArgLysValSerLysAlaGluAlaAaGlnGluAsnAlaSer 196  
Db 243 ATGATATATTGCTACAGAAAGGTCTCAAAAGCCGAGAGGAGCCCAAGAAAACCGCTCT 302  
Qy 197 AspTyrLeuAlaIleProSerGluAsnLysGluAsnSerAlaValProValGluGlu 215  
Db 303 GACTACCTTGCCATCCATCTGAGAACCAAGAGAACTCTGCGGTACCACTGAGGAGAA 359

## RESULT 13

US-10-029-191-23  
; Sequence 23, Application US/10029191  
; Publication No. US20020160453A1  
; GENERAL INFORMATION:

; APPLICANT: CURTIS, ROY A.J.  
; TITLE OF INVENTION: NOVEL GENE ENCODING A SODIUM CHANNEL BETA-3 SUBUNIT  
; FILE REFERENCE: 210147.00XX/SUI  
; CURRENT APPLICATION NUMBER: US/10/029,191  
; PRIOR FILING DATE: 2001-12-20  
; PRIOR APPLICATION NUMBER: 09/569,978  
; PRIOR FILING DATE: 2000-05-12  
; PRIOR APPLICATION NUMBER: US 60/134,198  
; PRIOR FILING DATE: 1999-05-14  
; NUMBER OF SEQ ID NOS: 23  
; SOFTWARE: Patent In Ver. 2.1  
; SEQ ID NO 23  
; LENGTH: 657  
; TYPE: DNA  
; ORGANISM: Lepus Sp.  
US-10-029-191-23

Alignment Scores:  
Pred. No.: 9,498-55 Length: 657  
Score: 477.00 Matches: 106  
Percent Similarity: 64.49% Conservative: 32  
Best Local Similarity: 49.53% Mismatches: 68  
Query Match: 42.44% Indels: 8  
DB: 5 Gaps: 5

US-09-977-579A-2 (1-215) x US-10-029-191-23 (1-657)

Qy 10 LeuAlaSerLeuValLeuIleTyrTrpValSerValCysPheProValCysValGluVal 29  
Db 13 CTGGCTTTCTGTTGGTGGCGCGCTGTGTCTCGGCTGGGGGGCTGGGTGGAGGTG 72  
Qy 30 ProSerGluThrGluAlaValGlnGlyAsnProMetLysLeuArgCysIleSerCysMet 49  
Db 73 GACTCGGAGACCGGAGCGCTGTACGGGATGACCTTCANAAATCTCTGTGATCTCTCTGCAAG 132  
Qy 50 LysArgGluGluValGluAlaThrValValGluTrpPheThrArgProGluGlyGly 69  
Db 133 CGCCGACGAGACCGACCGCGGAGACCTTCACGGAGTGGACCTTCGCGCAGAAAGGCGACT 192  
Qy 70 LysAspPheLeu---IleTyrGluTyrArgAsnGlyHisGlnGluValGluSerPro--- 87  
Db 193 GAGGAGTTCTGTCAGAGATCTCGCTATGAGAACGAGGTGCTGCACTGGAGGAGAACGAG 252  
Qy 88 ---PheGlnGlyArgGluTrpAsnGlySer-----LysAspLeuGlnAspVal 103  
Db 253 CGCTTTTGAGGGCGCGCTGTGTGGNACCGGAGCGGGGACCAAGGACCTTCAGGACCTG 312  
Qy 104 SerIleThrValLeuAsnValThrLeuAsnAspSerglyLeuTyrThrCysAsnValSer 123  
Db 313 TCCATCTTCATCACCACATGTCACTTACCAACCACTCGGGCGACTACCACTGCTCTAC 372  
Qy 124 ArgGluPheGluPheGluAlaHisArgProPheValLysThrArgLeuIleProLeu 143  
Db 373 CGCTCTGCTCTCTCGAAACCTACGAGCACCAACACCGCGCTCGTCAAGAGATCCACCTG 432  
Qy 144 ArgValThrGluGluAlaGlyGluAspPheThrSerValValSerGluIleMetMetTyr 163  
Db 433 GAGGTGGTGGACAGGCCAACAGAGACATGCGCATCATCGTGTCCGAGATCATGATGTAC 492  
Qy 164 IleLeuLeuValPheLeuThrLeuTrpLeuLeuIleGluMetIleTyrCysTyrArgLys 183  
Db 493 GTGCTCATCGTGGTGTTCACCATCTGGCTCGTGGCGGAGATGGTGTACTGTCTACAAGAG 552  
Qy 184 ValSerLysAla---GluGluAlaAlaGlnGluAsnAlaSerAspTyrLeuAlaIlePro 202  
Db 553 ATCGCGCGCGCCACCGAGGACGCGCGGAGAGAACGCTCTCGGAATACTTGGCCATCACC 612  
Qy 203 SerGluAsnLysGluAsn---SerAlaValProValGluGlu 215  
Db 613 TCAGAAAGCAAGAAATTTGACACGGGCGTCCAGGTGGGTGAA 654

RESULT 14

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US-10-723-860-2247
; Sequence 2247, Application US/10723860
; Publication No. US2004025360A1
; GENERAL INFORMATION:
; APPLICANT: Aziz, Natasha
; APPLICANT: Gineburg, Wendy M.
; APPLICANT: Zlotnik, Albert
; TITLE OF INVENTION: Methods for Screening for Soft Tissue Sarcoma Modulators
; TITLE OF INVENTION: Methods for Screening for Soft Tissue Sarcoma Modulators
; FILE REFERENCE: 03882.0193.NPUS01
; CURRENT APPLICATION NUMBER: US/10723.860
; PRIOR FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: 60/429,739
; PRIOR FILING DATE: 2002-11-26
; NUMBER OF SEQ ID NOS: 8393
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2247
; LENGTH: 1335
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-723-860-2247

Alignment Scores:
Pred. No.: 1.01e-53 Length: 1335
Score: 473.00 Matches: 109
Percent Similarity: 63.35% Conservative: 31
Best Local Similarity: 49.32% Mismatches: 71
Query Match: 42.08% Indels: 10
DB: 8 Gaps: 6

US-09-977-579A-2 (1-215) x US-10-723-860-2247 (1-1335)

Qy 3 AlaPheAsnArgLeuPheProLeuAlaSerLeuValLeuIleTyrTrpValSerValCys 22
Db 22 GCCATTGGGGAGGCTG-----CTGGCTTAGTGGCGCGGCGGCACTGGTGTCTCAGCC 75
Qy 23 PheProValCysValGluValProSerGluThrGluAlaValGlnGlyAsnProMetLys 42
Db 76 TCGGGGGGCTCGTGGAGGTGGACTCGAGACCAGCGCGGTGTATGGGATGACCTTCAAA 135
Qy 43 LeuArgCysIleSerCysMetLysArgGluGluValGluAlaThrValGluTrp 62
Db 136 ATTCTTTGCATCTCTCGAAGCGCGGAGCGAGACCAAGCTGAGACCTTACCAGGTGG 195
Qy 63 PheTyrArgProGluGlyGlyLysAspPheLeu---IleTyrGluTyrArgAsnGlyHis 81
Db 196 ACCTTCGCCCAAGAGGCACTGAGGAGTTTGTCAAGATCTCTGCGCTATGAGAATGAGGTG 255
Qy 82 GlnGluValGluSerPro-----PheGlnGlyArgLeuGlnTrpAsnGlySer----- 97
Db 256 TTGCAGCTGGAGGAGGATGAGCGCTTCAGGGCGCGCGTGGTGTGGAATGGAGCGCGGGC 315
Qy 98 ---LysAspLeuGlnAspValSerIleThrValLeuAsnValThrLeuAsnAspSerGly 116
Db 316 ACCAAGACCTGCGAGGATCTCTATCTCATCACCAATGTCTACCTACACCACTCGGCG 375
Qy 117 LeuTyrThrCysAenValSerArgGluPheGluAlaHisArgProPheValLys 136
Db 376 GACTACGAGTGCCACGCTCTACCGCTCTCTTCTCGAATACTACGAGCAACACACGAGC 435
Qy 137 ThrThrArgLeuIleProLeuArgValThrGluGluAlaGlyGluAspPheThrSerVal 156
Db 436 GTCGTCAAGAGATCCCATTTGAGGTAGTGAGCAAGAGCCAAACAGAGACATGGCATCCATC 495
Qy 157 ValSerGluIleMetMetTyrIleLeuLeuValPheLeuThrLeuLeuLeuGlu 176
Db 496 GTGCTGAGATCATGATGATGTCTCATTTGTGTGTGGTGTGACCATATGGCTCGTGGCAGAG 555
Qy 177 MetIleTyrCysTyrArgLysValSerLysAla---GluGluAlaAlaGlnGluAsnAla 195
Db 556 ATGATTTACTCTCAAGAGATCGCTGCCCGCAGGAGACTGCTGCACAGGAGATGCC 615
Qy 196 SerAspTyrLeuAlaIleProSerGluAsnLysGluAsn---SerAlaValProValGlu 214
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Db 616 TCGAATACCTGGCCATCACCTCTGAAAGCAAGAGAACTGCACGGCGTCCAGGTGGCC 675
Qy 215 Glu 215
Db 676 GAA 678

RESULT 15
US-10-477-272-1
; Sequence 1, Application US/10477272
; Publication No. US20040191791A1
; GENERAL INFORMATION:
; APPLICANT: Bionomics Limited
; TITLE OF INVENTION: P12
; FILE REFERENCE: SCNIB (R85C)
; CURRENT APPLICATION NUMBER: US/10/477,272
; CURRENT FILING DATE: 2003-11-10
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 1414
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-477-272-1

Alignment Scores:
Pred. No.: 1.1e-53 Length: 1414
Score: 473.00 Matches: 109
Percent Similarity: 63.35% Conservative: 31
Best Local Similarity: 49.32% Mismatches: 71
Query Match: 42.08% Indels: 10
DB: 8 Gaps: 6

US-09-977-579A-2 (1-215) x US-10-477-272-1 (1-1414)

Qy 3 AlaPheAsnArgLeuPheProLeuAlaSerLeuValLeuIleTyrTrpValSerValCys 22
Db 98 GCCATTGGGGAGGCTG-----CTGGCTTAGTGGTGGCGCGGCACTGGTGTCTCAGCC 151
Qy 23 PheProValCysValGluValProSerGluThrGluAlaValGlnGlyAsnProMetLys 42
Db 152 TCGGGGGGCTCGCTGGAGGTGGACTCGAGACCAGCGCGGTGTATGGGATGACCTTCAAA 211
Qy 43 LeuArgCysIleSerCysMetLysArgGluGluValGluAlaThrValGluTrp 62
Db 212 ATTCTTTGCATCTCTCGAAGCGCGGAGCGGAGACCAAGCTGAGACCTTACCAGGTGG 271
Qy 63 PheTyrArgProGluGlyGlyLysAspPheLeu---IleTyrGluTyrArgAsnGlyHis 81
Db 272 ACCTTCGCCCAAGGAGGCACTGAGGAGTTTGTCAAGATCTCTGCGCTATGAGAATGAGGTG 331
Qy 82 GlnGluValGluSerPro-----PheGlnGlyArgLeuGlnTrpAsnGlySer----- 97
Db 332 TTGCAGCTGGAGGAGGATGAGTGTTCGAGGGCGCGGTGGTGTGGAATGGAGCGCGGGC 391
Qy 98 ---LysAspLeuGlnAspValSerIleThrValLeuAsnValThrLeuAsnAspSerGly 116
Db 392 ACCAAGACCTGCGAGGATCTCTATCTCATCACCAATGTCTACCTACACCACTCGGCG 451
Qy 117 LeuTyrThrCysAsnValSerArgGluPheGluAlaHisArgProPheValLys 136
Db 452 GACTACGAGTGCCACGCTCTACCGCTCTCTTCTCGAATACTACGAGCAACACACGAGC 511
Qy 137 ThrThrArgLeuIleProLeuArgValThrGluGluAlaGlyGluAspPheThrSerVal 156
Db 512 GTCGTCAAGAGATCCCATTTGAGGTAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 571
Qy 157 ValSerGluIleMetMetTyrIleLeuLeuValPheLeuThrLeuLeuLeuGlu 176
Db 572 GTGCTGAGATCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 631
Qy 177 MetIleTyrCysTyrArgLysValSerLysAla---GluGluAlaAlaGlnGluAsnAla 195
```

Db	632	ATGATTTACTGCTACAAAGAGATCGCTGCGCCACGGAGACTGTGCTCACAGGAGATGCC	691
Qy	196	SerAspTyrLeuAlaIleProSerGluAsnLysGluAsn---SerAlaValProValGlu	214
Db	692	TCGGATACCTGGCCATCACCTCTGAAAGCAAGAGAACTGCACGGGCGTCCAGGTGCC	751
Qy	215	Glu	215
Db	752	GAA	754

Search completed: January 5, 2006, 19:11:07  
Job time : 788 secs

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GenCore version 5.1.6  
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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: January 5, 2006, 16:44:17 ; Search time 203 Seconds  
(without alignments)  
772.027 Million cell updates/sec

Title: US-09-977-579A-2  
Perfect score: 1124  
Sequence: 1 MPAENRLLPLASULVLIYVWS.....SDYLAIPSENKENSAPVEE 215

Scoring table:  
BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 4637609 seqs, 364468668 residues

Total number of hits satisfying chosen parameters: 9275218

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

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-Q=/cgn2\_1/USPTO.spool/US09977579/runat 05012006.160655.29045/app query.fasta\_1.391  
-DB=Published Applications NA New -QFMT=fastap -SUFFIX=rnpbn -MINMATCH=0.1  
-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62  
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100  
-THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0  
-MAXLEN=2000000000 -USER=US09977579 @CGN 1.1 122 @runat 05012006.160655.29045  
-NCPU=6 -ICPU=3 -NO WMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100  
-LONGLOG -DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5  
-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Published Applications NA New.\*

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2: /cgn2\_6/ptodata/1/pubpna/US06 NEW PUB.seq.\*  
3: /cgn2\_6/ptodata/1/pubpna/US07 NEW PUB.seq.\*  
4: /cgn2\_6/ptodata/1/pubpna/PCT NEW PUB.seq.\*  
5: /cgn2\_6/ptodata/1/pubpna/US09 NEW PUB.seq.\*  
6: /cgn2\_6/ptodata/1/pubpna/US10 NEW PUB.seq.\*  
7: /cgn2\_6/ptodata/1/pubpna/US11 NEW PUB.seq.\*  
8: /cgn2\_6/ptodata/1/pubpna/US11 NEW PUB.seq2.\*  
9: /cgn2\_6/ptodata/1/pubpna/US11 NEW PUB.seq3.\*  
10: /cgn2\_6/ptodata/1/pubpna/US60 NEW PUB.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1124	100.0	1261	US-10-374-954-8	Sequence 8, Appli
2	1105	98.3	3820	US-11-136-527-750	Sequence 750, App
3	473	42.1	1335	US-10-374-954-4	Sequence 4, Appli
4	472	42.0	1400	US-11-136-527-6498	Sequence 6498, Ap
5	472	42.0	1490	US-10-533-355-7	Sequence 7, Appli
6	472	42.0	1508	US-11-136-527-2402	Sequence 2402, Ap
7	241	21.4	880	US-10-750-185-44336	Sequence 44336, A
8	241	21.4	880	US-10-750-623-44336	Sequence 44336, A

9	165.5	14.7	150468	7	US-11-112-908-56	Sequence 56, Appl
10	165.5	14.7	193789	7	US-11-112-908-55	Sequence 55, Appl
11	147	13.1	673	7	US-11-080-991-111	Sequence 111, Appl
12	147	13.1	1371	6	US-10-131-826A-487	Sequence 487, App
13	131	11.7	1777	6	US-10-131-826A-529	Sequence 529, App
14	114	10.1	1015	6	US-11-136-527-2158	Sequence 2158, Ap
15	110.5	9.8	648	6	US-10-374-954-6	Sequence 6, Appli
16	109	9.7	1630	6	US-10-131-826A-519	Sequence 519, App
17	108.5	9.7	2458	6	US-10-131-826A-387	Sequence 387, App
18	105	9.3	1497	6	US-10-750-185-44339	Sequence 44339, A
19	105	9.3	1497	6	US-10-750-623-44339	Sequence 44339, A
20	102.5	9.1	138821	7	US-11-121-086-80	Sequence 80, Appl
21	100	8.9	600	7	US-11-136-527-6254	Sequence 6254, Ap
22	99.5	8.9	1324	6	US-10-750-185-44343	Sequence 44343, A
23	99.5	8.9	1324	6	US-10-750-623-44343	Sequence 44343, A
24	98.5	8.8	396	6	US-10-959-310-22	Sequence 22, Appl
25	98.5	8.8	433	7	US-11-012-353-62	Sequence 62, Appl
26	98.5	8.8	433	7	US-11-012-353-66	Sequence 66, Appl
27	96.5	8.6	2749	6	US-10-131-826A-385	Sequence 385, App
28	95.5	8.5	2311	7	US-11-136-527-3513	Sequence 3513, Ap
29	94.5	8.4	2793	6	US-10-775-169-228	Sequence 228, App
30	93.5	8.3	396	6	US-10-932-334-49	Sequence 49, Appl
31	93.5	8.3	1506	6	US-10-750-185-30397	Sequence 30397, A
32	93.5	8.3	1506	6	US-10-750-623-30397	Sequence 30397, A
33	93	8.3	2906	6	US-10-131-826A-367	Sequence 367, App
34	92.5	8.2	393	6	US-10-789-273-33	Sequence 13, Appl
35	92.5	8.2	393	7	US-11-125-837-31	Sequence 31, Appl
36	92	8.2	1116	7	US-11-087-177-38	Sequence 38, Appl
37	90	8.0	1326	6	US-10-055-877-76	Sequence 76, Appl
38	90	8.0	1650	7	US-11-000-688-144	Sequence 144, App
39	90	8.0	2473	7	US-11-080-991-77	Sequence 77, Appl
40	90	8.0	2537	7	US-11-102-978-8	Sequence 8, Appli
41	90	8.0	162085	7	US-11-121-086-7	Sequence 7, Appli
42	89.5	8.0	438	7	US-11-012-353-48	Sequence 48, Appl
43	89	7.9	1077	7	US-11-136-527-613	Sequence 613, App
44	89	7.9	3286	7	US-11-136-527-158	Sequence 158, App
45	89	7.9	54946	6	US-10-995-561-13479	Sequence 13479, A

#### ALIGNMENTS

RESULT 1  
US-10-374-954-8  
; Sequence 8, Application US/10374954  
; Publication No. US20050260576A1  
; GENERAL INFORMATION:  
; APPLICANT: Vanderbilt University  
; APPLICANT: George, Alfred L  
; APPLICANT: Lossin, Christoph  
; TITLE OF INVENTION: HETEROLOGOUS EXPRESSION SYSTEM FOR STUDYING RECOMBINANT HUMAN  
; FILE REFERENCE: 1242/41/2  
; CURRENT APPLICATION NUMBER: US/10/374,954  
; CURRENT FILING DATE: 2003-02-25  
; PRIOR APPLICATION NUMBER: US 60/359,382  
; PRIOR FILING DATE: 2002-02-25  
; NUMBER OF SEQ ID NOS: 27  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 8  
; TYPE: DNA  
; LENGTH: 1261  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (376)..(1023)  
US-10-374-954-8  
Alignment Scores:  
Pred. No.: 8.27e-139  
Score: 1124.00  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Length: 1261  
Matches: 215  
Conservative: 0  
Mismatches: 0  
Indels: 0

DB: 6 Gaps: 0

US-09-977-579A-2 (1-215) x US-10-374-954-8 (1-1261)

Qy 1 MetProAlaPheAsnArgLeuPheProLeuAlaSerLeuValLeuIleTyrTrpValSer 20  
376 ATGCTGCCCTTCATAGATTGTTCCCTGGCTTCTCTCGTCTTACTACTGGGTCACT 435

Qy 21 ValCysPheProValCysValGluValProSerGluThrGluAlaValGlnGlyAsnPro 40  
436 GTCTGCTTCCCTGTGTGTGGAAGTGCCTTCGAGACGAGGCGGTGCAGGGCAACCCC 495

Qy 41 MetLysLeuArgCysIleSerCysMetLysArgGluValGluAlaThrValVal 60  
496 ATGAAGCTGGCTGCATCTCTCATGAAGAGAGAGGAGGTGGAGGCCACACCGTGGTG 555

Qy 61 GluTrpPheTyrArgProGluGlyGlyLysAspPheLeuIleTyrGluTyrArgAsnGly 80  
556 GAATGGTCTACAGCCCGAGGGCGGTAAAGATTTCCTTATTACAGATATCGGAATGGC 615

Qy 81 HisGlnGluValGluSerProPheGlnGlyArgLeuGlnTrpAsnGlySerLysAspLeu 100  
616 CACCAGAGGTGGAGAGCCCTTTTCAGGGCGCTGCGAGTGAATGGCAGCAGGACCTG 675

Qy 101 GlnAspValSerIleThrValLeuAsnValThrLeuAsnAspSerGlyLeuTyrThrCys 120  
676 CAGACGTGTCCATCACTGTGCTCAACGTCACTCTGAACGACTCTGGCCTCTACACCTGC 735

Qy 121 AsnValSerArgGluPheGluAlaHisArgProPheValLysThrThrArgLeu 140  
736 AATGTGTCCCGGAGTTTGAGTTGAGCGCATCGGCCCTTTGTGAAGACGACGCGCTG 795

Qy 141 IleProLeuArgValThrGluGluAlaGlyGluAspPheThrSerValValSerGluIle 160  
796 ATCCCTTAAAGTCAACGAGGAGGCTGGAGAGACTTCACCTGTGTGCTTCAGAAATC 855

Qy 161 MetMetTyrIleLeuLeuValPheLeuThrLeuTrpLeuIleGluMetIleTyrCys 180  
856 ATGATGTACATCTCTGTGCTTCTCCACCTGTGGCTGCTCATCGAGATGATATATGC 915

Qy 181 TyrArgLysValSerLysAlaGluGluAlaGlnGluAsnAlaSerAspTyrLeuAla 200  
916 TACAGAAAGTCTCAAAAGCCGAGAGGAGCCCAAGAAACGCTGTGACTACCTTGCC 975

Qy 201 IleProSerGluAsnLysGluAsnSerAlaValProValGluGlu 215  
976 ATCCCATCTGAGAACAAAGGAGAACTCTGCGGTACCACTGGAGGAA 1020

RESULT 2

US-11-136-527-750

; Sequence 750, Application US/11136527

; Publication No. US20050287570A1

; GENERAL INFORMATION:

; APPLICANT: Wyeth

; APPLICANT: Mounts, William M

; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes

; FILE REFERENCE: 031896-041000 (AM101086)

; CURRENT APPLICATION NUMBER: US/11/136,527

; CURRENT FILING DATE: 2005-05-25

; PRIOR APPLICATION NUMBER: US 60/574,294

; PRIOR FILING DATE: 2005-05-26

; NUMBER OF SEQ ID NOS: 362830

; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 750

; LENGTH: 3820

; TYPE: DNA

; ORGANISM: Rattus norvegicus

US-11-136-527-750

Alignment Scores:

Pred. No.: 1.54e-135 Length: 3820

Score: 1105.00 Matches: 211

Percent Similarity: 98.14% Conservative: 0

Best Local Similarity: 98.14% Mismatches: 4

Query Match: 98.31% Indels: 0

DB: 7 Gaps: 0

US-09-977-579A-2 (1-215) x US-11-136-527-750 (1-3820)

Qy 1 MetProAlaPheAsnArgLeuPheProLeuAlaSerLeuValLeuIleTyrTrpValSer 20  
363 ATGCTGCCCTTCACAGATTGCTTCCCTAGCTTCTCTAGTCTCATCTACTGGTTCAGA 422

Qy 21 ValCysPheProValCysValGluValProSerGluThrGluAlaValGlnGlyAsnPro 40  
423 GTCTGCTTCCCTGTGTGTGGAAGTGCCTTCGAGACAGAGCGGTGCAGGGCAATCCC 482

Qy 41 MetLysLeuArgCysIleSerCysMetLysArgGluValGluAlaThrValVal 60  
483 ATGAAGCTGAGGTGCATCTCTCATGAAGAGGAGGAGGTGGAGGCCACACCTGTGGTG 542

Qy 61 GluTrpPheTyrArgProGluGlyGlyLysAspPheLeuIleTyrGluTyrArgAsnGly 80  
543 GAGTGGTCTACAGGCTTGAAGCGGTAAAGATTTCCTTATATATAGATATCGGAATGGC 602

Qy 81 HisGlnGluValGluSerProPheGlnGlyArgLeuGlnTrpAsnGlySerLysAspLeu 100  
603 CACCAGAGGTGGAGAGCCCTTCCAGGCGCTCTGCAGTGAATGGGAGCAAGACCTG 662

Qy 101 GlnAspValSerIleThrValLeuAsnValThrLeuAsnAspSerGlyLeuTyrThrCys 120  
663 CAGGACGTATCCATCACTGTACTCAATGTCACTTGAATGACTCTGGCCTCTACACATGC 722

Qy 121 AsnValSerArgGluPheGluAlaHisArgProPheValLysThrThrArgLeu 140  
723 AATGTGTCCAGGAGTTTGAATTCGAGGCAACAGGCCCTTTGTGAAGACACGAGACTG 782

Qy 141 IleProLeuArgValThrGluGluAlaGlyGluAspPheThrSerValValSerGluIle 160  
783 ATACCTTTGCGAGTCACTGAAGAGGCGGAGAGACTTCACCTCCGTGGTCTCGAAATC 842

Qy 161 MetMetTyrIleLeuLeuValPheLeuThrLeuTrpLeuIleGluMetIleTyrCys 180  
843 ATGATGTACATCTCTCGTGGTCTTCCACCTGTGGCTGTTTATTGAGATGATCTATTGC 902

Qy 181 TyrArgLysValSerLysAlaGluGluAlaGlnGluAsnAlaSerAspTyrLeuAla 200  
903 TACAGAAAGTCTCTAAGCGCGAGAGGAGCAGCAGGAAATGCGTCTGACTACTTGTCT 962

Qy 201 IleProSerGluAsnLysGluAsnSerAlaValProValGluGlu 215  
963 ATCCCTTCAGAGAACAGGAGAACTCTGTGGTACCTGTGGAGGAA 1007

RESULT 3

US-10-374-954-4

; Sequence 4, Application US/10374954

; Publication No. US20050260576A1

; GENERAL INFORMATION:

; APPLICANT: Vanderbilt University

; APPLICANT: George, Alfred L

; APPLICANT: Lossin, Christoph

; TITLE OF INVENTION: HETEROLOGOUS EXPRESSION SYSTEM FOR STUDYING RECOMBINANT HUMAN

; TITLE OF INVENTION: BRAIN VOLTAGE-GATED SODIUM CHANNEL, SCN1A

; FILE REFERENCE: 1242/41/2

; CURRENT APPLICATION NUMBER: US/10/374,954

; CURRENT FILING DATE: 2003-02-25

; PRIOR APPLICATION NUMBER: US 60/359,382

; PRIOR FILING DATE: 2002-02-25

; NUMBER OF SEQ ID NOS: 27

; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 4

; LENGTH: 1335

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: CDS



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; LOCATION: (25)...(681)
; US-10-374-954-4
Alignment Scores:
Pred. No.: 3.89e-52 Length: 1335
Score: 473.00 Matches: 109
Percent Similarity: 63.35% Conservative: 31
Best Local Similarity: 49.32% Mismatches: 71
Query Match: 42.08% Indels: 10
DB: 6 Gaps: 6

US-09-977-579A-2 (1-215) x US-10-374-954-4 (1-1335)
Qy 3 AlaPheAnArgLeuPheProLeuAlaSerLeuValLeuLeuTyrTrpValSerValCys 22
Db 22 GCCATGGGGAGGCTG-----CTGGCTTAGTGGTCGGCGCGGCACTGGTCTCTCGAGCC 75
Qy 23 PheProValCysValGluValProSerGluThrGluAlaValGlnGlyAsnProMetLys 42
Db 76 TCGGGGGCTCGTGGAGTGGACTCGGAGACCGAGCGCGTGTATGGATGACCTTCAAA 135
Qy 43 LeuArgCysIleSerCysMetLysArgGluGluValGluAlaThrThrValValGluTrp 62
Db 136 ATTCTTTGCATCTCTCTCAAGCGCGCAGCGAGACCAACGCTGAGACCTTCCACGAGTGG 195
Qy 63 PheTyrArgProGluGlyCysAspPheLeu---IleTyrGluTyrArgAsnGlyHis 81
Db 196 ACCTTCCGCCAGAGGGCACTGAGGAGTTTGTCAAGATCTCTCGCGCTATGAGAATGAGGTG 255
Qy 82 GlnGluValGluSerPro-----PheGlnGlyArgLeuGlnTrpAsnGlySer----- 97
Db 256 TTGCAGCTGGAGGAGGATGAGCGCTTCAGGGCGCGTGGTGGAAATGGCAGCGCGGCG 315
Qy 98 ---LysAspLeuGlnAspValSerIleThrValLeuAsnValThrLeuAsnAspSerGly 116
Db 316 ACCAAGACCTGCAGGATCTGTCTATCTTCATCACCAGTGTCCACCTCAACACCTCGGGC 375
Qy 117 LeuTyrThrCysAsnValSerArgGluPheGluPheGluAlaHisArgProPheValLys 136
Db 376 GACTACGAGTGCACGCTACCGCTCTCTTTCGAAACTACGAGCACCAACACGAGC 435
Qy 137 ThrThrArgLeuIleProLeuArgValThrGluGluAlaGlyGluAspPheThrSerVal 156
Db 436 GTGCTCAGAGATCCATTCAGGTAGTGGCAAGCAAGCCACAGACATGTCATCCATC 495
Qy 157 ValSerGluIleMetMetTyrIleLeuLeuValPheLeuThrLeuTrpLeuLeuIleGlu 176
Db 496 GTGCTGAGATCATGATGATGTGCTCATTTGGTGGTTGACCATATGGCTCGTGCAGAG 555
Qy 177 MetIleTyrCysTyrArgLysValSerLysAla---GluGluAlaGlnGlnAsnAla 195
Db 556 ATGATTTACTGTACAAAGAGATCGTGCAGCGCAGGAGCTGTGCACAGAGAGATGCC 615
Qy 196 SerAspTyrLeuAlaIleProSerGluAsnLysGluAsn---SerAlaValProValGlu 214
Db 616 TCGGAATACCTGGCCATCACCTCTGAAAGCAAGAGAACTGCACGGCGCTCCAGTGGCC 675
Qy 215 Glu 215
Db 676 GAA 678

RESULT 4
US-11-136-527-6498
; Sequence 6498, Application US/11136527
; Publication No. US20050287570A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
; FILE REFERENCE: 031896-041000 (AM101086)
; CURRENT APPLICATION NUMBER: US/11/136,527
; CURRENT FILING DATE: 2005-05-25
; PRIOR APPLICATION NUMBER: US 60/574,294

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; PRIOR FILING DATE: 2005-05-26
; NUMBER OF SEQ ID NOS: 362830
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 6498
; LENGTH: 1400
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-11-136-527-6498
Alignment Scores:
Pred. No.: 5.69e-52 Length: 1400
Score: 472.00 Matches: 105
Percent Similarity: 64.49% Conservative: 33
Best Local Similarity: 49.07% Mismatches: 68
Query Match: 41.99% Indels: 8
DB: 7 Gaps: 5

US-09-977-579A-2 (1-215) x US-11-136-527-6498 (1-1400)
Qy 10 LeuAlaSerLeuValLeuIleTyrTrpValSerValCysPheProValCysValGluVal 29
Db 124 CTGGCTCTCGTGGTGGCGCGTGTCTGTATCTCTCAGCCTGGGGGGCTGGTGGAGGTG 183
Qy 30 ProSerGluThrGluAlaValGlnGlyAsnProMetLysLeuArgCysIleSerCysMet 49
Db 184 GATTCTGAGACCGAGGCGATGTATGGGATGACCTTCAAAATCTCTGTGTATCTCTGTAA 243
Qy 50 LysArgGluGluValGluAlaThrThrValValGluTyrPheTyrArgProGluGlyGly 69
Db 244 CGTCGTATGAGACCAACCGCGGAGACCTTCAGGAGTGGACCTTCGCGCAGAGGGCACA 303
Qy 70 LysAspPheLeu---IleTyrGluTyrArgAsnGlyHisGlnGluValGluSerPro--- 87
Db 304 CAGGAATTTGTCAAGATCTCTACGCTATGAGAATGAGGTGCTGCAGCTGGAGGAGATGAG 363
Qy 88 ---PheGlnGlyArgLeuGlnTrpAsnGlySer-----LysAspLeuGlnAspVal 103
Db 364 CGCTTTGAGGCGCGTGTGGTGGAAACGGTAGTTCGGGGCAGCAAGGACCTGCAGGACCTG 423
Qy 104 SerIleThrValLeuAsnValThrLeuAsnAspSerGlyLeuTyrThrCysAsnValSer 123
Db 424 TCCATCTTCATCACCACCAATGTCCCTTACCAACCACTCTGGCGACTACGAATGTCAGTCTAC 483
Qy 124 ArgGluPheGluPheGluAlaHisArgProPheValLysThrArgLeuIleProLeu 143
Db 484 CGTCTCTCTTCTTTGATAATTACGAGCACACACAGCGTCTCAAGAAGATCCACCTG 543
Qy 144 ArgValThrGluGluAlaGlyGluAspPheThrSerValSerValSerGluIleMetMetTyr 163
Db 544 GAGGTGGTGGACAGGCCAACAGAGATATGGCATCTCCATCGTGTCAAGATCATGTATGATAC 603
Qy 164 IleLeuLeuValPheLeuThrLeuTrpLeuLeuIleGluMetIleTyrCysTyrArgLys 183
Db 604 GTGCTCATTTGGTGTAAACCATATGGCTCTGGCGGAGATGGTGTACTCTCAAGAG 663
Qy 184 ValSerLysAla---GluGluAlaAlaGlnGluAsnAlaSerAspTyrIleuAlaIlePro 202
Db 664 ATTGCTGTGCCACCGAGCTGTGCACAGAGAAATGCTCGGAATACCTCGGCACTTACT 723
Qy 203 SerGluAsnLysGluAsn---SerAlaValProValGluGlu 215
Db 724 TCCGAGAGCAAGAGAACTGTACAGGCGTCCAGGCTGGCTGAA 765

RESULT 5
US-10-533-355-7
; Sequence 7, Application US/10533355
; Publication No. US20050272040A1
; GENERAL INFORMATION:
; APPLICANT: University of Medicine and Dentistry of New Jersey
; APPLICANT: Black, Ira B.
; TITLE OF INVENTION: A METHOD FOR INCREASING SYNAPTIC GROWTH OR PLASTICITY
; FILE REFERENCE: UMD-0016
; CURRENT APPLICATION NUMBER: US/10/533,355

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FILE REFERENCE: 031896-041000 (AM101086)  
 CURRENT APPLICATION NUMBER: US 60/422,986  
 PRIOR FILING DATE: 2002-11-01  
 NUMBER OF SEQ ID NOS: 16  
 SOFTWARE: PatentIn version 3.1  
 SEQ ID NO 7  
 LENGTH: 1490  
 TYPE: DNA  
 ORGANISM: Rattus norvegicus  
 US-10-533-355-7

Alignment Scores:  
 Pred. No.: 6,26e-52 Length: 1490  
 Score: 472.00 Matches: 105  
 Percent Similarity: 64.49% Conservative: 33  
 Best Local Similarity: 49.07% Mismatches: 68  
 Query Match: 41.99% Indels: 8  
 DB: Gaps: 5

US-09-977-579A-2 (1-215) x US-10-533-355-7 (1-1490)

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Qy 10 LeuAlaSerLeuValLeuIleTyrTrpValSerValCysPheProValCysValGluVal 29
Db 232 CTGGCTCTCGGTGGGGCGGCTGCTGATCTCTCAGCTGGGGGGCTGGTGGAGGTG 291
Qy 30 ProSerGluThrGluAlaValGlnGlyAsnProMetLysLeuArgCysIleSerCysMet 49
Db 292 GATTCTGAGACCGGAGGAGTGTATGGATGACCTTCAAAATCCTGTGTATCTCTCTGTAAG 351
Qy 50 LysArgGluGluValGluAlaThrValValGluTrpPheTyrArgProGluGlyGly 69
Db 352 CGTGTAGTGAGACCGCGGAGACCTTCACGAGTGGACCTTCGCCAGAGGGGACACA 411
Qy 70 LysAspPheLeu---IleTyrGluTyrArgAsnGlyHisGlnGluValGluSerPro--- 87
Db 412 GAGGAATTTGTCAAGATCTTACGCTATGAGATGAGGTGCTGCAGCTGGAGGAAGATGAG 471
Qy 88 ---PheGlnGlyArgLeuGlnTrpAsnGlySer-----LysAspLeuGlnAspVal 103
Db 472 CGCTTTGAGGCCGCTGTGTGTGGAACGGTAGTCCGGGGACCAAGGACCTGCAGGACCTG 531
Qy 104 SerIleThrValLeuAsnValThrLeuAsnAspSerGlyLeuTyrThrCysAsnValSer 123
Db 532 TCCATCTTCATCACCATTGTCACCTACACACTCTGCGGACTACGATGTCAGTCTAC 591
Qy 124 ArgGluPheGluPheGluAlaHisArgProPheValLysThrArgLeuIleProLeu 143
Db 592 CGTCTCTCTCTTTGATAATTACGAGCACAACACGAGCGTGGTCAAGAGATCCACCTG 651
Qy 144 ArgValThrGluGluAlaGlyLysAspPheThrSerValSerGluIleMetMetTyr 163
Db 652 GAGGTGTGGACAGGCCAACAGAGATATGCGATCCATCCATCGTGTGAGAGATCATGATGAC 711
Qy 164 IleLeuLeuValPheLeuThrLeuTrpLeuIleGluMetIleTyrCysTyrArgLys 183
Db 712 GTGCTCATTTGTGTGTAAACCATATGCTGTGGGAGATGGTGTACTGCTACAGAG 771
Qy 184 ValSerLysAla---GluGluAlaAlaGlnGluAsnAlaSerAspTyrLeuAlaIlePro 202
Db 772 ATTGCTGTCGCCAGGAAGCTGTGCACAAGAGATGCTCGGAATACCTGGCCATTACT 831
Qy 203 SerGluAsnLysGluAsn---SerAlaValProValGluGlu 215
Db 832 TCCGAGACCAAGAGAACTGTACAGGCGTCCAGGTGGCTGAA 873

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RESULT 6

US-11-136-527-2402  
 Sequence 2402, Application US/11136527  
 Publication No. US20050287570A1  
 GENERAL INFORMATION:  
 APPLICANT: Wyeth  
 APPLICANT: Mounts, William M  
 TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes

FILE REFERENCE: 031896-041000 (AM101086)  
 CURRENT APPLICATION NUMBER: US/11/136,527  
 PRIOR FILING DATE: 2005-05-25  
 PRIOR APPLICATION NUMBER: US 60/574,294  
 PRIOR FILING DATE: 2005-05-26  
 NUMBER OF SEQ ID NOS: 362830  
 SOFTWARE: PatentIn version 3.2  
 SEQ ID NO 2402  
 LENGTH: 1508  
 TYPE: DNA  
 ORGANISM: Rattus norvegicus  
 US-11-136-527-2402

Alignment Scores:  
 Pred. No.: 6,38e-52 Length: 1508  
 Score: 472.00 Matches: 105  
 Percent Similarity: 64.49% Conservative: 33  
 Best Local Similarity: 49.07% Mismatches: 68  
 Query Match: 41.99% Indels: 8  
 DB: Gaps: 5

```

US-09-977-579A-2 (1-215) x US-11-136-527-2402 (1-1508)
Qy 10 LeuAlaSerLeuValLeuIleTyrTrpValSerValCysPheProValCysValGluVal 29
Db 232 CTGGCTCTCGGTGGGGCGGCTGCTGATCTCTCAGCTGGGGGGCTGGTGGAGGTG 291
Qy 30 ProSerGluThrGluAlaValGlnGlyAsnProMetLysLeuArgCysIleSerCysMet 49
Db 292 GATTCTGAGACCGGAGGAGTGTATGGATGACCTTCAAAATCCTGTGTATCTCTCTGTAAG 351
Qy 50 LysArgGluGluValGluAlaThrValValGluTrpPheTyrArgProGluGlyGly 69
Db 352 CGTGTAGTGAGACCGCGGAGACCTTCACGAGTGGACCTTCGCCAGAGGGGACACA 411
Qy 70 LysAspPheLeu---IleTyrGluTyrArgAsnGlyHisGlnGluValGluSerPro--- 87
Db 412 GAGGAATTTGTCAAGATCTTACGCTATGAGATGAGGTGCTGCAGCTGGAGGAAGATGAG 471
Qy 88 ---PheGlnGlyArgLeuGlnTrpAsnGlySer-----LysAspLeuGlnAspVal 103
Db 472 CGCTTTGAGGCCGCTGTGTGTGGAACGGTAGTCCGGGGACCAAGGACCTGCAGGACCTG 531
Qy 104 SerIleThrValLeuAsnValThrLeuAsnAspSerGlyLeuTyrThrCysAsnValSer 123
Db 532 TCCATCTTCATCACCATTGTCACCTACACACTCTGCGGACTACGATGTCAGTCTAC 591
Qy 124 ArgGluPheGluPheGluAlaHisArgProPheValLysThrArgLeuIleProLeu 143
Db 592 CGTCTCTCTCTTTGATAATTACGAGCACAACACGAGCGTGGTCAAGAGATCCACCTG 651
Qy 144 ArgValThrGluGluAlaGlyLysAspPheThrSerValSerGluIleMetMetTyr 163
Db 652 GAGGTGTGGACAGGCCAACAGAGATATGCGATCCATCCATCGTGTGAGAGATCATGATGAC 711
Qy 164 IleLeuLeuValPheLeuThrLeuTrpLeuIleGluMetIleTyrCysTyrArgLys 183
Db 712 GTGCTCATTTGTGTGTAAACCATATGCTGTGGGAGATGGTGTACTGCTACAGAG 771
Qy 184 ValSerLysAla---GluGluAlaAlaGlnGluAsnAlaSerAspTyrLeuAlaIlePro 202
Db 772 ATTGCTGTCGCCAGGAAGCTGTGCACAAGAGATGCTCGGAATACCTGGCCATTACT 831
Qy 203 SerGluAsnLysGluAsn---SerAlaValProValGluGlu 215
Db 832 TCCGAGACCAAGAGAACTGTACAGGCGTCCAGGTGGCTGAA 873

```

RESULT 7

US-10-750-185-44336  
 Sequence 44336, Application US/10750185  
 Publication No. US20050260603A1  
 GENERAL INFORMATION:  
 APPLICANT: MMI GENOMICS, INC.



```

Qy      143 ----- 143
Db      59104 TCACACGAAGCTCAGACACACTCAGGCTGTCTATGAGCGCTGGCTTAAACC 59163
Qy      144 -ArgValThrGluGluAlaGlyGluAspPheThrSerValValSerGluIleMetMetTy 163
Db      59164 CTGCTGGCCCTCGACGCAACAGAGACATGGCATCTGCTGCTGAGATCATGATGTA 59223
Qy      163 rIleLeuLeuValPheLeuThrLeuTrpLeuLeuIleGluMetIleTyrCysTyrArgLy 183
Db      59224 TGTGCTCATTTGCTGTTGACCATATGGCTGCTGGCAGAGATGATTTACTGCTACAAGAA 59283
Qy      183 sValSerLyseAla---GluGluAlaAlaGlnGluAsnAla 195
Db      59284 GATCGCTGCCGCCACGAGAGACTGTGCACAGGAGATGCG 59323

RESULT 10
US-11-112-908-55
; Sequence 55, Application US/11112908
; Publication No. US20050260659A1
; GENERAL INFORMATION:
; APPLICANT: Harris, Cole
; APPLICANT: Davis, Lisa M.
; TITLE OF INVENTION: Breast Cancer Biomarkers
; FILE REFERENCE: 04-164-US
; CURRENT APPLICATION NUMBER: US/11/112,908
; CURRENT FILING DATE: 2005-04-22
; PRIOR APPLICATION NUMBER: US 60/564,758
; PRIOR FILING DATE: 2004-04-23
; PRIOR APPLICATION NUMBER: US 60/575,978
; PRIOR FILING DATE: 2004-06-01
; PRIOR APPLICATION NUMBER: US 60/631,702
; PRIOR FILING DATE: 2004-11-30
; PRIOR APPLICATION NUMBER: US 60/633,826
; PRIOR FILING DATE: 2004-12-07
; NUMBER OF SEQ ID NOS: 511
; SOFTWARE: Patent in version 3.3
; SEQ ID NO 55
; LENGTH: 193789
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-112-908-55

Alignment Scores:
Pred. No.:      6.96e-08      Length:      193789
Score:          165.50      Matches:      56
Percent Similarity: 47.13%      Conservative: 26
Best Local Similarity: 32.18%      Mismatches: 45
Query Match:     14.72%      Indels:      48
DB:              7          Gaps:       7

US-09-977-579A-2 (1-215) x US-11-112-908-55 (1-193789)
Qy      67 GluGlyGlyLysAspPheLeuIleTyrGlu-TyrArgAsnGlyHisGlnGluValGluSe 86
Db      108996 GAAGGAGGTATTCATTTTACAAATTGAAGAAACAGAGG-----CCTAGACACATTGATC 109049
Qy      86 rPropheGlnGlyArgLeu-----GlnTrp-----AsnGlySerLysAs 99
Db      109050 ACTTGGCGAAGTTCACACAGCTGGCCAGTGGCAGCGCCCTTTGAACCTGAGCCTTCT 109109
Qy      99 pLeuGlnAspValSerIle-----ThrValLeuAsnValThrLeuAsnAspSerGlyLe 117
Db      109110 GGTTCAGAGCTACGGCTTTTAGGCACCGTGTGAGCGCCCTCCAG-AATGACACAGATGT 109168
Qy      117 uTyrThrCysAsnValSerArgGluPheGluPheGluAlaHisArg----- 132
Db      109169 GGCCTCGAGTTACACAGGAGGCGAGGTGAGGGTGACCCCAACAGCCTTACCAAGGCT 109228
Qy      133 -----ProPheValLysThrArgIleProLeu----- 143
Db      109229 GGGTATTAAATACAGTGCATACACAGGCCCGGAGGGTTGAGCCACTCATCCAAGC 109288

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Qy      143 ----- 143
Db      109289 TCACACGAAGCTCAGACACACTCAGGCTGTCTATGAGCGCTGGCTTAAACC 109348
Qy      144 -ArgValThrGluGluAlaGlyGluAspPheThrSerValValSerGluIleMetMetTy 163
Db      109349 CTGCTGGCCCTCGACGCAACAGAGACATGGCATCTGCTGCTGAGATCATGATGTA 109408
Qy      163 rIleLeuLeuValPheLeuThrLeuTrpLeuLeuIleGluMetIleTyrCysTyrArgLy 183
Db      109409 TGTGCTCATTTGCTGTTGACCATATGGCTGCTGGCAGAGATGATTTACTGCTACAAGAA 109468
Qy      183 sValSerLyseAla---GluGluAlaAlaGlnGluAsnAla 195
Db      109469 GATCGCTGCCGCCACGAGAGACTGTGCACAGGAGATGCG 109508

RESULT 11
US-11-080-991-111
; Sequence 111, Application US/11080991
; Publication No. US20050266437A1
; GENERAL INFORMATION:
; APPLICANT: Veiby, Petter Ole
; TITLE OF INVENTION: COMPOSITIONS, KITS, AND METHODS FOR
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF BREAST
; TITLE OF INVENTION: AND OVARIAN CANCER
; FILE REFERENCE: MRI-039
; CURRENT APPLICATION NUMBER: US/11/080,991
; CURRENT FILING DATE: 2005-03-11
; PRIOR APPLICATION NUMBER: US/10/176,847
; PRIOR FILING DATE: 2002-06-21
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 111
; LENGTH: 673
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-080-991-111

Alignment Scores:
Pred. No.:      3.28e-09      Length:      673
Score:          147.00      Matches:      57
Percent Similarity: 41.44%      Conservative: 35
Best Local Similarity: 25.68%      Mismatches: 80
Query Match:     13.08%      Indels:      50
DB:              7          Gaps:       9

US-09-977-579A-2 (1-215) x US-11-080-991-111 (1-673)
Qy      7 LeuPheProLeuAlaSerLeuValLeuIleTyrTrpValSerValCysPheProValCys 26
Db      89 CTTTGGCCTATAGCAGCT---GTGGAAATTTATACCTCCCGGTG----- 130
Qy      27 ValGluValProSerGluThrGluAlaValGlnGlyAsnProMetLysLeuArgCysIle 46
Db      131 -----CTGGAGGCTGTTAATGGGACAGATGCTCGGTTAAATGACT 172
Qy      47 SerCysMetLysArgGluGluValGluAlaThrThrValValGluTrpPheTyrArgPro 66
Db      173 TTCTCCAGCTTTGCCCTGCTGGGTGATGCTCTAAACAGTGACC---TGGAAATTTTCGTCT 229
Qy      67 ---GluGlyGly---LysAspPheLeuIleTyrGluTyrArgAsnGlyHisGlnGluVal 84
Db      230 CTAGACGGGGGAGCCTGAGCAGTTTGTATTCTTACCAACATAGATCCTCTTCCAAACCCATG 289
Qy      85 GluSerProPheGlnGlyArgLeuGlnTrpAsnGlySerLysAspLeuGlnAspValSer 104
Db      290 AGTGGGGCGGTTTAAAGNCCGGGTCTTGGGATGGGAATCCTGAGCGGTACGATGCCTCC 349
Qy      105 IleThrValLeuAsnValThrLeuAsnAspSerGlyLeuTyrThrCysAsnValSerArg 124
Db      350 ATCTCTCTCTGGAAACCTGAGTTTCACGACCAATGGGACATACACCTGCCAGGTGAAGAAC 409

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Qy 125 GluPheGluPheGluAlaHisArgProPheValIleThrThrArgLeuIleProLeuArg 144  
Db 410 -----CCACCTGAT 418  
Qy 145 ValThrGluGluAlaGlyGluAspPheThrSerValVal-----SerGlu 159  
Db 419 GTTGATGGGTGATAGGGGAGATCCGGCTCAGCGTCGTGCACACTGTACGCTTCTCTGAG 478  
Qy 160 IleMetMetTyrIleLeuLeuVal-----PheLeuThrLeuTrpLeu 173  
Db 479 ATCCACTTCTCGCTCTGGCTTGGCTCTGCCTGTGCACACTGATCATATAAGTAATT 538  
Qy 174 LeuIleGluMetIleTyrCysTyrArgLysValSerLysAlaGluGluAlaGlnGlu 193  
Db 539 GTAGTGGTCTCTTCCACCATTTACCGAAAGCGATGGCGGAAAGAGCT----- 589  
Qy 194 AsnAlaSerAspTyrLeuAlaIleProSerGluAsnLysGluAsnSerAlaValProVal 213  
Db 590 -----CATAAAGTGTGGAGATAAAATCAAAAGAGAGAGAAAGGCTCAACCAA 637  
Qy 214 GluGlu 215  
Db 638 GAGAAA 643

## RESULT 12

US-10-131-826A-487  
; Sequence 487, Application US/10131826A  
; Publication No. US20050245730A1  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Beresini, Maureen  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Sherwood, Steven  
; APPLICANT: Smith, Victoria  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Watanabe, Colin K  
; APPLICANT: Wood, William  
; APPLICANT: Zhang, Zemin  
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
; TITLE OF INVENTION: ACIDS ENCODING THE SAME  
; FILE REFERENCE: P3330R1C128  
; CURRENT APPLICATION NUMBER: US/10/131,826A  
; CURRENT FILING DATE: 2002-04-24  
; PRIOR APPLICATION NUMBER: 60/049911  
; PRIOR FILING DATE: 1997-06-18  
; PRIOR APPLICATION NUMBER: 60/056974  
; PRIOR FILING DATE: 1997-08-26  
; PRIOR APPLICATION NUMBER: 60/059113  
; PRIOR FILING DATE: 1997-09-17  
; PRIOR APPLICATION NUMBER: 60/059115  
; PRIOR FILING DATE: 1997-09-17  
; PRIOR APPLICATION NUMBER: 60/059117  
; PRIOR FILING DATE: 1997-09-17  
; PRIOR APPLICATION NUMBER: 60/059122  
; PRIOR FILING DATE: 1997-09-17  
; PRIOR APPLICATION NUMBER: 60/059184  
; PRIOR FILING DATE: 1997-09-17  
; PRIOR APPLICATION NUMBER: 60/059263  
; PRIOR FILING DATE: 1997-09-18  
; PRIOR APPLICATION NUMBER: 60/059352  
; PRIOR FILING DATE: 1997-09-19  
; PRIOR APPLICATION NUMBER: 60/059588  
; PRIOR FILING DATE: 1997-09-19  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 550

; SEQ ID NO 487  
; LENGTH: 1371  
; TYPE: DNA  
; ORGANISM: Homo Sapien  
US-10-131-826A-487  
Alignment Scores:  
Pred. No.: 9.8e-09 Length: 1371  
Score: 147.00 Matches: 57  
Percent Similarity: 41.44% Conservative: 35  
Best Local Similarity: 25.68% Mismatches: 80  
Query Match: 13.08% Indels: 50  
DB: Gaps: 9

US-09-977-579A-2 (1-215) x US-10-131-826A-487 (1-1371)

Qy 7 LeuPheProLeuAlaSerLeuValLeuIleTyrTrpValSerValCysPheProValCys 26  
Db 181 CTTTGGCTATAGCAGCT---GTGGAATTTATACCTCCCGGGTG----- 222  
Qy 27 ValGluValProSerGluThrGluAlaValGlnGlyAsnProMetLysLeuArgCysIle 46  
Db 223 -----CTGGAGCGCTGTTAATGGGACAGATGCTCGGTTAAATGCAC 264  
Qy 47 SerCysMetLysArgGluGluValGluAlaThrThrValValGluTrpPheTyrArgPro 66  
Db 265 TTCTCCAGCTTTGCCCTGTGGGTGATGCTCTAACAGTGACC---TGGAAATTTGCTCCT 321  
Qy 67 ---GluGlyGly---LysAspPheLeuIleTyrGluTyrArgAsnGlyHisGlnGluVal 84  
Db 322 CTAGACGGGGACCTGAGCAGTTTGTATTCTACTACCAATAGATCCCTTCCACCCCATG 381  
Qy 85 GluSerProPheGlnGlyArgLeuLysTrpAsnGlySerLysAspLeuGluAspValSer 104  
Db 382 AGTGGCGGTTTAAAGCACCGGGTGTCTTGGGATGGGAATCTCTGACGCTACGATGCCTCC 441  
Qy 105 IleThrValLeuAsnValThrLeuAsnAspSerGlyLeuTyrThrCysAsnValSerArg 124  
Db 442 ATCCTTCTCTCGAAACTTCAGCTTCGACGACAATGGGACATACACCTGCAGGTGAAGAAC 501  
Qy 125 GluPheGluPheGluAlaHisArgProPheValLysThrArgLeuIleProLeuArg 144  
Db 502 -----CCACCTGAT 510  
Qy 145 ValThrGluGluAlaGlyGluAspPheThrSerValVal-----SerGlu 159  
Db 511 GTTGATGGGTGATAGGGGAGATCCGGCTCAGCGCTCGTGCACACTGTACGCTTCTCTGAG 570  
Qy 160 IleMetMetTyrIleLeuLeuVal-----PheLeuThrLeuTrpLeu 173  
Db 571 ATCCACTTCTCGCTCTGGCCATTGGCTCTGCCTGTGCACATGATCATATAAGTAATT 630  
Qy 174 LeuIleGluMetIleTyrCysTyrArgLysValSerLysAlaGluGluAlaGlnGlu 193  
Db 631 GTAGTGGTCTCTTCCACCATTTACCGGAAAGCGATGGCGGAAAGAGCT----- 681  
Qy 194 AsnAlaSerAspTyrLeuAlaIleProSerGluAsnLysGluAsnSerAlaValProVal 213  
Db 682 -----CATAAAGTGTGGAGATAAAATCAAAAGAGAGAGAAAGGCTCAACCAA 729  
Qy 214 GluGlu 215  
Db 730 GAGAAA 735

## RESULT 13

US-10-131-826A-529  
; Sequence 529, Application US/10131826A  
; Publication No. US20050245730A1  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Beresini, Maureen  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: DeForge, Laura  
; APPLICANT: Desnoyers, Luc



Qy	82	GlnGluValGluSerPropheGlnGlyArgLeuGlnTrpAsnGlySerLysAspLeuGln	101
Dd	434	CTGAAGCTGGAGCGG---TTTGGACACCGGTAGAGTTCTCGGGGAACCCCAAGAATAC	490
Qy	102	AspValSerIleThrValLeuAasnValThrLeuAasnAspSerGlyLeuTyThrCysAasn	121
Dd	491	GACGTGTCAGTGACTCTAAAGAACGTCGCAGCTAGAAAGACGAAGGCATTTACAACTCGTAC	550
Qy	122	ValSerArgGluPheGluPheGluAlaHisArgPropheValLysThrThrArgLeuIle	141
Dd	551	ATCACCAAC-----CCTCCAGACCGCCACCCTGGCCCATGCCAAGATCTTACCTGCAGGTC	604
Qy	142	ProLeuArgValThrGluGluAlaGlyGluaspPheThrSerValValSerGluIleMet	161
Dd	605	CTTCTWGAAGTGCCTCCCAGAGCGRCAKCKCAGCGTGGCGAGTCATCTGTGGTGCCCTCAGTG	664
Qy	162	MettYrIleLeuLeuValPheLeuThrLeuTrpLeuLeuIleGluMetIleTyrcystyr	181
Dd	665	GGGGGTTTCCTGRCRTGTGGTCATM-----TTRGTCGTATGGTGGTCAAATGTGNG	715
Qy	182	ArgLysValserLysAlaGluAlaLaGlnGluAasnAlaSerAspTyrrLeuAlaIle	201
Dd	716	AGGAGG-----AAAAAGAGCAGAGAAGCTGAGCAGCGATCACYTGAAGACC	760
Qy	202	ProSerGluAasnLysGluAasnSerAlaValProValGluGlu	215
Dd	761	GAAGAGGAGGCGAAGCGGATCGCGAGGGCAACGGCGAAGAT	802

RESULT 15

US-10-374-954-6  
; Sequence 6, Application US/10374954  
; Publication No. US20050260576A1  
; GENERAL INFORMATION:  
; APPLICANT: Vanderbilt University  
; APPLICANT: George, Alfred L  
; APPLICANT: Loeisn, Christoph  
; TITLE OF INVENTION: HETEROLOGOUS EXPRESSION SYSTEM FOR STUDYING RECOMBINANT HUMAN  
; TITLE OF INVENTION: BRAIN VOLTAGE-GATED SODIUM CHANNEL, SCN1A  
; FILE REFERENCE: 1242/41/2  
; CURRENT APPLICATION NUMBER: US/10/374,954  
; CURRENT FILING DATE: 2003-02-25  
; PRIOR APPLICATION NUMBER: US 60/359,382  
; PRIOR FILING DATE: 2002-02-25  
; NUMBER OF SEQ ID NOS: 27  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 6  
; LENGTH: 648  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (1) .. (648)  
US-10-374-954-6

Alignment Scores:		
Pred. No.:	0.000222	Length:
Score:	110.50	Matches:
Percent Similarity:	45.33%	Conservative:
Best Local Similarity:	25.70%	Mismatches:
Query Match:	9.83%	Indels:
DP:	6	Gaps:
		11
		648

US-09-977-579A-2 (1-215) x US-10-374-954-6 (1-648)

[illegible]

Qy	39	AsnProMetLysIleuArgCysValle-----SerCysMetLysArgGluGluValGluAla	56
Dd	130	TCTGACGCCCGCCCTGCAGCCTTCAACTTCCTGTACACAGTAGAACCAACAACAGTTC	189
Qy	57	ThrThrValValGluTrpPheTyrrArgProGluGlyGly-----LysAspPheLeu	73
Dd	190	TCC-----CTGAACCTGGACTTACCAGGAGTGCAACAACACTGCTCTGAGGAGATGTTCTCTC	243
Qy	74	IleTyrgLuTyrrArgAnsnGlyHisGlnGluValGluserrProPheGlnGlyArgLeuGln	93
Dd	244	CAGTTCGCGCATGAAGAATCATTAACCTGAAGCTGGAGCGG---TTTTCAAGACCGCGTGGAG	300
Qy	94	TriAsnGlySerLysAspLeuGlnAspValSerIleThrValLeuAsnValThrLeuAsn	113
Dd	301	TTCTCAGGAAACCCAGCAAGTACGATGTGTGCGTGATGCTGAGAAAAGTGTCAGCGCGGAG	360
Qy	114	AspSergIleuTyrrThrCysAsnValSerArgGluPheGluPheGluAlaHisArgPro	133
Dd	361	GATCAGGGGATTTCACACTGCTATCATCATGAAC-----CCCCCTGACGCCACCAGTGGC	414
Qy	134	PheValLysThrThrArgLeuIleProLeuArgValThrGluGluAlaGlyLeuAspPhe	153
Dd	415	CATGGCAAG-----ATCCATCTGCAGGTCTCTCATGGAGAGAGCCCCTGAGCGG	462
Qy	154	ThrSerValValSerGluIleMetMetTyrrIleLeuLeuValPheLeuThrLeuTrpLeu	173
Dd	463	GACTCCACGGTGGCGGTGATTGTGGGTGCCCTCCGTCGGGGGGCTTCTGCTGTGGTCATC	522
Qy	174	LeuIleGluMetIleTyrr---CysTyrrArgLysValSerLysAalaGluGluAlaAaGln	192
Dd	523	TTGTGCTGATGGTGGTCAAGTGTGTGAGGAGA-----AAAAAAGAGCAG	567
Qy	193	GluAsnAlaSerAspTyrrLeuAlaIleProSerGluAsnLys	206
Dd	568	AAGCTTGACCAAGATGACCTCAAGACCGGAGGAGGGCGCAAG	609

Search completed: January 5, 2006, 17:54:07  
Job time : 269 secs



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